

WO 2005/037989

PCT/US2003/024918

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ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggt 480
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<210> 148
<211> 499
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse-Human hybrid fusion protein

<400> 148
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Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
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Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

35 40 45
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 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
 130 135 140 145
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser Cys
 260 265 270
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 275 280 285
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 290 295 300
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 305 310 315 320
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 325 330 335
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 340 345 350
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 355 360 365
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 370 375 380
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 385 390 395 400
 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 405 410 415
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 420 425 430 435
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 440 445 450
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 455 460 465
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 470 475 480
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 485 490 495
 Pro Gly Lys

<210> 149

<211> 1470

<212> DNA

<213> Artificial Sequence

<220>

<223> Mouse-Human hybrid fusion protein

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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aatatgcact gggtaaaaga gacacctaga cagggcctgg aatggattgg agctatttat 600
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<210> 150

<211> 482

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse-Human hybrid fusion protein

<400> 150

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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
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Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20      25      30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35      40      45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50      55      60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65      70      75      80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85      90      95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100     105     110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115     120     125
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
130     135     140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145     150     155     160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165     170     175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180     185     190     195
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
200     205     210
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
215     220     225
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
230     235     240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245     250     255
Gly Thr Gly Thr Thr Val Thr Val Ser Asp Pro Arg Arg Leu Asp Lys

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 275 280 285
 Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser Leu Leu Asn Cys
 290 295 300
 Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys Asp Ile Met Leu
 305 310 315 320
 Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu Met Gln Lys Gly
 325 330 335
 Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser
 340 345 350
 Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met
 355 360 365
 Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys
 370 375 380
 Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn
 385 390 395 400
 Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys
 405 410 415
 Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr His
 420 425 430
 Ser Ser Ala Lys Pro Cys Gly Gln Ser Ile His Leu Gly Gly Val
 435 440 445
 Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro
 450 455 460
 Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys
 465 470 475 480
 Leu Glu

<210> 151

<211> 1290

<212> DNA

<213> Artificial Sequence

<220>

<223> Mouse-Human hybrid fusion protein

<400> 151

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 ccaggggaga aggtcacat aattgtcagg gccagctcaa gtgtaagtta catgactgg 180
 taccagagata agccaggatt ctcgccaaa ccttggaatt atgcccatt caactgggt 240
 tctggagttc ctgctcgttt cagtggcagt gggtctggga cctcttact tctcaaat 300
 agcagagtgg aggtgaaga tgcgtccact tattactgcc agcagtgag tttaacca 360
 cccacgtctg gtgctgggac caagctggag ctgaagggtg gcggtggctt gggcgggtgt 420
 ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggtc tgagctgggt 480
 aggcctgggg cctcagtgaa gatgtcctgc aaggcttctg gctacacatt taccagttac 540
 aatatgcact gggtaaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600
 ccaggaaatg gtgatacttc ctacaatcag aagtccaagg gcaaggccac actcagtgtg 660
 gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgct 720
 gcttatttct gtgcaagagt ggtgttactat agtaactctt actggtactt cgatgtctgg 780
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<210> 152

<211> 422

<212> PRT

<213> Artificial Sequence

<220>

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
<223> Mouse-Human hybrid fusion protein

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<400> 152
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Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Glu Asp Ala Thr Tyr Tyr Cys Gln Leu Trp
100 105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Thr Lys
115 120 125
Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
130 135 140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145 150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165 170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
210 215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225 230 235 240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245 250 255
Gly Thr Gly Thr Thr Val Thr Val Ser Asp Pro Glu Asn Ser Phe Glu
260 265 270
Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser
275 280 285
Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly
290 295 300
Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln
305 310 315 320
Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr
325 330 335
Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser
340 345 350
Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala
355 360 365
Ala Asn Thr His Ser Ser Ala Pro Cys Gly Gln Gln Ser Ile His
370 375 380
Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn
385 390 395 400
Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe
405 410 415
Gly Leu Leu Lys
420

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<210> 153
<211> 3630
<212> DNA
<213> Homo sapiens

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<400> 153
atacggggaga actaaggctg aaacctcgga ggaacaacca cttttgaagt gacttcgcgg 60
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cgcgcgctg agaaccgccc ggaacgcacg tgggcgcgcg gcgttcccc cgttccacg 180
gtgggcgcg gccgccaggc caccacagt ccggcccccg ggatgcgcgt cctcctgcc 240

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

35 40 45

Pro Met Gly Leu Phe Pro Thr Gln Gln Cys Pro Gln Arg Pro Thr Asp
50 55 60

Cys Arg Lys Gln Cys Glu Pro Asp Tyr Tyr Leu Asp Glu Ala Asp Arg
65 70 75

Cys Thr Ala Cys Val Thr Cys Ser Arg Asp Asp Leu Val Glu Lys Thr
85 90 95

Pro Cys Ala Trp Asn Ser Ser Arg Val Cys Glu Cys Arg Pro Gly Met
100 105 110

Phe Cys Ser Thr Ser Ala Val Asn Ser Cys Ala Arg Cys Phe Phe His
115 120 125

Ser Val Cys Pro Ala Gly Met Ile Val Lys Phe Gly Thr Ala Gln
130 135 140

Lys Asn Thr Val Cys Glu Pro Ala Ser Pro Gly Val Ser Pro Ala Cys
145 150 155 160

Ala Ser Pro Glu Asn Cys Lys Glu Pro Ser Ser Gly Thr Ile Pro Gln
165 170 175

Ala Lys Pro Thr Pro Val Ser Pro Ala Thr Ser Ser Ala Ser Thr Met
180 185 190

Pro Val Arg Gly Gly Thr Arg Leu Ala Gln Glu Ala Ala Ser Lys Leu
195 200 205

Thr Arg Ala Pro Asp Ser Pro Ser Val Gly Arg Pro Ser Ser Asp
210 215 220

Pro Gly Leu Ser Pro Thr Gln Pro Cys Pro Glu Gly Ser Gly Asp Cys
225 230 235 240

Arg Lys Gln Cys Glu Pro Asp Tyr Tyr Leu Asp Glu Ala Gly Arg Cys
245 250 255

Thr Ala Cys Val Ser Cys Ser Arg Asp Asp Leu Val Glu Lys Thr Pro
260 265 270

Cys Ala Trp Asn Ser Ser Arg Thr Cys Glu Cys Arg Pro Gly Met Ile
275 280 285

Cys Ala Thr Ser Ala Thr Asn Ser Cys Ala Arg Cys Val Pro Tyr Pro
290 295 300

Ile Cys Ala Ala Glu Thr Val Thr Lys Pro Gln Asp Met Ala Glu Lys
305 310 315 320

Asp Thr Thr Phe Glu Ala Pro Pro Leu Gly Thr Gln Pro Asp Cys Asn
325 330 335

Pro Thr Pro Glu Asn Gly Glu Ala Pro Ala Ser Thr Ser Pro Thr Gln
340 345 350

Ser Leu Leu Val Asp Ser Gln Ala Ser Lys Thr Leu Pro Ile Pro Thr
355 360 365

Ser Ala Pro Val Ala Leu Ser Thr Gly Lys Pro Val Leu Asp Ala
370 375 380

Gly Pro Val Leu Phe Trp Val Ile Leu Val Leu Val Val Val Gly
385 390 395 400

Ser Ser Ala Phe Leu Leu Cys His Arg Arg Ala Cys Arg Lys Arg Ile
405 410 415

Arg Gln Lys Leu His Leu Cys Tyr Pro Val Gln Thr Ser Gln Pro Lys
420 425 430

Leu Glu Leu Val Asp Ser Arg Pro Arg Arg Ser Ser Thr Gln Leu Arg
435 440 445

Ser Gly Ala Ser Val Thr Glu Pro Val Ala Glu Glu Arg Gly Leu Met
450 455 460

Ser Gln Pro Leu Met Glu Thr Cys His Ser Val Gly Ala Ala Tyr Leu
465 470 475 480

Glu Ser Leu Pro Leu Gln Asp Ala Ser Pro Ala Gly Gly Pro Ser Ser
485 490 495

Pro Arg Asp Leu Pro Glu Pro Arg Val Ser Thr Glu His Thr Asn Asn
500 505 510

Lys Ile Glu Lys Ile Tyr Ile Met Lys Ala Asp Thr Val Ile Val Gly
515 520 525

Thr Val Lys Ala Glu Leu Pro Glu Gly Arg Gly Leu Ala Gly Pro Ala
530 535 540

Glu Pro Glu Leu Glu Glu Glu Leu Glu Ala Asp His Thr Pro His Tyr
545 550 555 560

Pro Glu Gln Glu Thr Glu Pro Pro Leu Gly Ser Cys Ser Asp Val Met
565 570 575

Leu Ser Val Glu Glu Glu Gly Lys Asp Pro Leu Pro Thr Ala Ala
580 585 590

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
ser Gly Lys
595

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<210> 155
<211> 1824
<212> DNA
<213> Homo sapiens

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aaaaaaaaa aaaaaaaaaa aaaaaaaa aaaaaaaa aaaaaaaa aaaaaaaa 1824

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<210> 156
<211> 547
<212> PRT
<213> Homo sapiens

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<400> 156
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Leu Leu Arg Val Glu Pro Gln Asn Pro Val Leu Ser Ala Gly Gly Ser
35 40 45
Leu Phe Val Asn Cys Ser Thr Asp Cys Pro Ser Ser Glu Lys Ile Ala
50 55 60
Leu Glu Thr Ser Leu Ser Lys Glu Leu Val Ala Ser Gly Met Gly Trp
65 70 75 80
Ala Ala Phe Asn Leu Ser Asn Val Thr Gly Asn Ser Arg Ile Leu Cys
85 90 95
Ser Val Tyr Cys Asn Gly Ser Gln Ile Thr Gly Ser Ser Asn Ile Thr
100 105 110
Val Tyr Gly Leu Pro Glu Arg Val Glu Leu Ala Pro Leu Pro Trp
115 120 125
Gln Pro Val Gly Gln Asn Phe Thr Leu Arg Cys Gln Val Glu Gly Gly
130 135 140
Ser Pro Arg Thr Ser Leu Thr Val Val Leu Leu Arg Trp Glu Glu Glu
145 150 155 160
Leu Ser Arg Gln Pro Ala Val Glu Glu Pro Ala Glu Val Thr Ala Thr

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
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 195 200 205
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 210 215 220
 Leu Val Ala Pro Arg Phe Leu Glu Val Glu Thr Ser Trp Pro Val Asp
 225 230 235 240
 Cys Thr Leu Asp Gly Leu Phe Pro Ala Ser Glu Ala Gln Val Tyr Leu
 245 250 255
 Ala Leu Gly Asp Gln Met Leu Asn Ala Thr Val Met Asn His Gly Asp
 260 265 270
 Thr Leu Thr Ala Thr Ala Thr Ala Arg Ala Asp Gln Glu Gly
 275 280 285
 Ala Arg Glu Ile Val Cys Asn Val Thr Leu Gly Gly Arg Arg Glu
 290 295 300
 Ala Arg Glu Asn Leu Thr Val Phe Ser Phe Leu Gly Pro Ile Val Asn
 305 310 315 320
 Leu Ser Glu Pro Thr Thr Ala His Glu Gly Ser Thr Val Thr Val Ser Cys
 325 330 335
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 <211> 199
 <212> PRT
 <213> Homo sapiens

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 5 Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Cys Val
 10 Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
 15 Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
 20 Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
 25 Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
 30 Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
 35 His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
 40 Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
 45 Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
 50 Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser
 55 Arg Leu Thr Asp Val Thr Leu
 60 195

<210> 163
 <211> 822
 <212> DNA
 <213> Homo sapiens

<400> 163
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 ccacttggtt aaggtgtatg actatcaaga agatggtctg gctacttcta cttgtgatgc 180
 agaagcAAA aatatcacat ggtttaaaga tgggaagatg atcggtcttc taactgaaga 240
 taaaaaaaa tggaaacttg gaagtaatgc agagaccctc cgagggatgt atcagtgtaa 300
 aggatcacag acaagttcaa aaccactcca agtgtattac agaatgtgtc agaactgcac 360
 tgaactaaat gcagccacca tatctggctt tctctttgct gaaatcgta gccatttctg 420

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<210> 164
<211> 182
<212> PRT
<213> Homo sapiens

<400> 164
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20 25 30
Val Tyr Asp Tyr Gln Glu Asp Gly Ser Val Leu Leu Thr Cys Asp Ala
35 40 45
Glu Ala Lys Asn Ile Thr Trp Phe Lys Asp Gly Lys Met Ile Gly Phe
50 55 60
Leu Thr Gly Asp Lys Lys Trp Asn Leu Gly Ser Asn Ala Lys Asp
65 70 75 80
Pro Arg Gly Met Tyr Gln Cys Lys Gly Ser Gln Asn Lys Ser Lys Pro
85 90 95
Leu Gln Val Tyr Tyr Arg Met Cys Gln Asn Cys Ile Glu Leu Asn Ala
100 105 110
Ala Thr Ile Ser Gly Phe Leu Phe Ala Glu Ile Val Ser Ile Phe Val
115 120 125
Leu Ala Val Gly Val Tyr Phe Ile Ala Gly Gln Asp Gly Val Arg Gln
130 135 140
Ser Arg Ala Ser Asp Lys Gln Thr Leu Leu Pro Asn Asp Gln Leu Tyr
145 150 155 160
Gln Pro Leu Lys Asp Arg Glu Asp Asp Gln Tyr Ser His Leu Gln Gly
165 170 175
Asn Gln Leu Arg Arg Asn
180

<210> 165
<211> 1311
<212> DNA
<213> Homo sapiens

<400> 165
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tagtgtaatg aagaaaatggg ttgtattaca cagacaccat ataaagtctc catctctgga 180
accacagtaa tattgacatg ccttcagtat cctggatctg aaatactatg gcaacacaat 240
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<210> 166
<211> 207
<212> PRT
<213> Homo sapiens

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20      25      30
Gln Thr Pro Tyr Lys Val Ser Ile Ser Gly Thr Thr Val Ile Leu Thr
35      40      45
Cys Pro Gln Tyr Pro Gly Ser Glu Ile Leu Trp Gln His Asn Asp Lys
50      55      60
Asn Ile Gly Gly Asp Glu Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp
65      70      75      80
His Leu Ser Leu Lys Glu Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr
85      90      95
Val Cys Tyr Pro Arg Gly Ser Lys Pro Glu Asp Ala Asn Phe Tyr Leu
100     105     110
Tyr Leu Arg Ala Arg Val Cys Glu Asn Cys Met Glu Met Asp Val Met
115     120     125
Ser Val Ala Thr Ile Val Ile Val Asp Ile Cys Ile Thr Gly Gly Leu
130     135     140
Leu Leu Leu Val Tyr Tyr Trp Ser Lys Asn Arg Lys Ala Lys Ala Lys
145     150     155     160
Pro Val Thr Arg Gly Ala Gly Ala Gly Arg Gln Arg Gly Gln Asn
165     170     175
Lys Glu Arg Pro Pro Pro Val Pro Asn Pro Asp Tyr Glu Pro Ile Arg
180     185     190
Lys Gly Gln Arg Asp Leu Tyr Ser Gly Leu Asn Gln Arg Arg Ile
195     200     205

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<210> 167
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<212> DNA
<213> Homo sapiens - to be filled in

<220>
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<223> n = A,T,C or G

<400> 167
nnn

3

<210> 168
<211> 2
<212> PRT
<213> Homo sapiens - to be filled in

<220>
<221> VARIANT
<222> 1, 2
<223> Xaa = Any Amino Acid

<400> 168
Xaa Xaa
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<210> 169
<211> 3084
<212> DNA
<213> Homo sapiens

<400> 169
ctgggtctcct ggttgacagag ctccaagtcc tcacacagat acgcctgttt gagaagcagc 60

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<210> 170
 <211> 458
 <212> PRT
 <213> Homo sapiens

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 20 25 30
 Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser Gln Lys Gly Ser
 35 40 45
 Ile Gln Phe His Trp Lys Asn Ser Asn Gln Ile Lys Ile Leu Gly Asn
 50 55 60
 Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser Lys Leu Asn Asp Arg Ala
 65 70 75 80
 Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe Pro Leu Ile Ile

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 Asp Gln Lys Glu Glu Val Gln Leu Leu Val Phe Gly Leu Thr Ala Asn
 115 120 125
 Ser Asp Thr His Leu Leu Gln Gly Gln Ser Leu Thr Leu Thr Leu Glu
 130 135 140
 Ser Pro Pro Gly Ser Ser Pro Ser Val Gln Cys Arg Ser Pro Arg Gly
 145 150 155 160
 Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser Val Ser Gln Leu Glu Leu
 165 170 175
 Gln Asp Ser Gly Thr Trp Thr Cys Thr Val Leu Asn Gln Lys Lys
 180 185 190
 Val Glu Phe Lys Ile Asp Ile Val Val Leu Ala Phe Gln Lys Ala Ser
 195 200 205
 Ser Ile Val Tyr Lys Lys Glu Gly Gln Val Glu Phe Ser Phe Pro
 210 215 220
 Leu Ala Phe Thr Val Glu Lys Leu Thr Gly Ser Gly Glu Leu Trp Trp
 225 230 235 240
 Gln Ala Glu Arg Ala Ser Ser Ser Lys Ser Trp Ile Thr Phe Asp Leu
 245 250 255
 Lys Asn Lys Glu Val Ser Val Lys Arg Val Thr Gln Asp Pro Lys Leu
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 275 280 285
 Pro Gln Tyr Ala Gly Ser Gly Asn Leu Thr Leu Ala Leu Glu Ala Lys
 290 295 300
 Thr Gly Lys Leu His Gln Glu Val Asn Leu Val Met Arg Ala Thr
 305 310 315 320
 Gln Leu Gln Lys Asn Leu Thr Cys Glu Val Trp Gly Pro Thr Ser Pro
 325 330 335
 Lys Leu Met Leu Ser Leu Lys Leu Glu Asn Lys Glu Ala Lys Val Ser
 340 345 350
 Lys Arg Glu Lys Ala Val Trp Val Leu Asn Pro Glu Ala Gly Met Trp
 355 360 365
 Gln Cys Leu Leu Ser Asp Ser Gly Gln Val Leu Leu Glu Ser Asn Ile
 370 375 380
 Lys Val Leu Pro Thr Trp Ser Thr Pro Val Gln Pro Met Ala Leu Ile
 385 390 395 400
 Val Leu Gly Gly Val Ala Gly Leu Leu Phe Ile Gly Leu Gly Ile
 405 410 415
 Phe Phe Cys Val Arg Cys Arg His Arg Arg Gln Ala Glu Arg Met
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<210> 171
 <211> 2308
 <212> DNA
 <213> Homo sapiens

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Cys Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr
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Trp Thr Gln Pro Gln Leu Ile Cys Thr Gly Glu Met Glu Thr Ser Gln
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 50 55 60
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 65 70 75
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http://www.uspto.gov/patent

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<212> PRT

<213> Homo sapiens

<400> 178

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Gly Ala Ala Gln Val Pro Ala Gln Leu Leu Val Gly Ala Leu Arg Val
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145 150 155 160
Leu Ala Glu Leu Gln Gln Trp Leu Lys Pro Gly Leu Lys Val Leu Ser
165 170 175
Ile Ala Gln Ala His Ser Pro Ala Phe Ser Cys Glu Gln Val Arg Ala
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Phe Pro Ala Leu Thr Ser Leu Asp Leu Ser Asp Asn Pro Gly Leu Gly
195 200 205
Glu Arg Gly Leu Met Ala Ala Leu Cys Pro His Lys Phe Pro Ala Ile
210 215 220
Gln Asn Leu Ala Leu Arg Asn Thr Gly Met Glu Thr Pro Thr Gly Val
225 230 235 240
Cys Ala Ala Leu Ala Ala Ala Gly Val Gln Pro His Ser Leu Asp Leu
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Ser His Asn Ser Leu Arg Ala Thr Val Asn Pro Ser Ala Pro Arg Cys
260 265 270
Met Trp Ser Ser Ala Leu Asn Ser Leu Asn Leu Ser Phe Ala Gly Leu
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Glu Gln Val Pro Lys Gly Leu Pro Ala Lys Leu Arg Val Leu Asp Leu
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Ser Cys Asn Arg Leu Asn Arg Ala Pro Gln Pro Asp Glu Leu Pro Glu
305 310 315 320
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325 330 335
Ala Leu Pro His Glu Gly Ser Met Asn Ser Gly Val Val Pro Ala Cys
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<211> 2633

<212> DNA

<213> Homo sapiens

<400> 179

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<212> PRT
<213> Homo sapiens

<400> 180
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35 40 45
Asp Lys Asp Ile Ser Trp Phe Ser Pro Asn Gly Glu Lys Leu Thr Pro
50 55 60
Asn Gln Gln Arg Ile Ser Val Trp Asn Asp Ser Ser Ser Thr
65 70 75
Leu Thr Ile Tyr Asn Ala Asn Ile Asp Asp Ala Gly Ile Tyr Lys Cys
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Val Val Thr Gly Glu Asp Gly Ser Glu Ser Glu Ala Thr Val Asn Val
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Lys Ile Phe Gln Lys Leu Met Phe Lys Asn Ala Pro Thr Pro Gln Glu
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Phe Arg Glu Gly Glu Asp Ala Val Ile Val Cys Asp Val Val Ser Ser
130 135 140
Leu Pro Pro Thr Ile Ile Trp Lys His Lys Gly Arg Asp Val Ile Leu
145 150 155
Lys Lys Asp Val Arg Phe Ile Val Leu Ser Asn Asn Tyr Leu Gln Ile
160 165 170 175
Arg Gly Ile Lys Lys Thr Asp Glu Gly Thr Tyr Arg Cys Glu Gly Arg
180 185 190
Ile Leu Ala Arg Gly Glu Ile Asn Phe Lys Asp Ile Gln Val Ile Val
195 200 205
Asn Val Pro Pro Thr Ile Arg Ala Arg Gln Asn Ile Val Asn Ala Thr
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Ala Asn Leu Gly Gln Ser Val Thr Leu Val Cys Asp Ala Glu Arg Phe
225 230 235 240
Pro Glu Pro Thr Met Ser Trp Thr Lys Asp Gly Glu Gln Ile Glu Gln
245 250 255
Glu Glu Asp Asp Glu Lys Tyr Ile Phe Ser Asp Asp Ser Ser Gln Leu
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Ser Thr Ala Gln Val Gln Phe Asp Glu Pro Glu Ala Thr Gly Gly Val
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Pro Ile Leu Lys Tyr Lys Ala Glu Trp Arg Ala Val Gly Glu Glu Val
530 535 540
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545 550 555 560
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595 600 605
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Gln Asp Asp Gly Gly Ser Pro Ile Arg His Tyr Leu Val Arg Tyr Arg
625 630 635 640
Ala Leu Ser Ser Glu Trp Lys Pro Glu Ile Arg Leu Pro Ser Gly Ser
645 650 655 660
Asp His Val Met Leu Lys Ser Leu Asp Trp Asn Ala Glu Tyr Gly Val
665 670 675
Tyr Val Val Ala Glu Asn Gln Gln Gly Lys Ser Lys Ala Ala His Phe
680 685 690
Val Phe Arg Thr Ser Ala Gln Pro Thr Ala Ile Pro Ala Asn Gly Ser
695 700 705
Pro Thr Ser Gly Leu Ser Thr Gly Ala Ile Val Gly Ile Leu Ile Val
710 715 720
Ile Phe Val Leu Leu Val Val Val Asp Ile Thr Cys Tyr Phe Leu
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Asn Lys Cys Gly Leu Phe Met Cys Ile Ala Val Asn Leu Cys Gly Lys
740 745 750
Ala Gly Pro Gly Ala Lys Gly Lys Asp Met Glu Glu Gly Lys Ala Ala
755 760 765
Phe Ser Lys Asp Glu Ser Lys Glu Pro Ile Val Glu Val Arg Thr Glu
770 775 780
Glu Glu Arg Thr Pro Asn His Asp Gly Gly Lys His Thr Glu Pro Asn
785 790 800
Glu Thr Thr Pro Leu Thr Glu Pro Glu Lys Gly Pro Val Glu Ala Lys
805 810 815
Pro Glu Cys Gln Glu Thr Glu Thr Lys Pro Ala Pro Glu Val Lys
820 825 830
Thr Val Pro Asn Asp Ala Thr Gln Thr Lys Glu Asn Glu Ser Lys Ala
835 840 845

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<211> 199
<212> PRT
<213> Homo sapiens

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35 40 45
Val Phe Ile Thr Ile Leu Ile Ile Ala Leu Ile Ala Leu Ser Val Gly
50 55 60
Gln Tyr Asn Cys Pro Gly Gln Tyr Thr Phe Ser Met Pro Ser Asp Ser
65 70 75 80
His Val Ser Ser Cys Ser Glu Asp Trp Val Gly Tyr Gln Arg Lys Cys
85 90 95
Tyr Phe Ile Ser Thr Val Lys Arg Ser Trp Thr Ser Ala Gln Asn Ala
100 105 110
Cys Ser Glu His Gly Ala Thr Leu Ala Val Ile Asp Ser Glu Lys Asp
115 120 125
Met Asn Phe Leu Lys Arg Tyr Ala Gly Arg Glu Glu His Trp Val Gly
130 135 140
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145 150 155 160
Phe Asn Asn Trp Phe Asn Val Thr Gly Ser Asp Lys Cys Val Phe Leu
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Lys Asn Thr Glu Val Ser Ser Met Glu Cys Glu Lys Asn Leu Tyr Trp
180 185 190
Ile Cys Asn Lys Pro Tyr Lys

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<213> Homo sapiens

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<210> 184
<211> 208
<212> PRT
<213> Homo sapiens

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35 40 45
Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg
50 55 60
Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg Val Asp
65 70 75 80
Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly Glu Glu Asp
85 90 95
Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly Lys Asp Trp
100 105 110
Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys Ile Asp Ser
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130 135 140
Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr Val Ala His
145 150 155 160
Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala Asp Leu
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<212> DNA
<213> Homo sapiens

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aagataataa cggaaaaaaa aaaaaaaaaa aaaaaa 1440

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<210> 186
<211> 312
<212> PRT
<213> Homo sapiens

<400> 186
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1 5 10 15
Leu Phe Val Glu Ser Ser Leu Asp Lys Val Val Leu Ser Asp Ala Tyr
20 25 30
Ala His Pro Gln Gln Lys Val Ala Val Tyr Arg Ala Leu Gln Ala Ala
35 40 45
Leu Ala Glu Ser Gly Gly Ser Pro Asp Val Leu Gln Met Leu Lys Ile
50 55 60
His Arg Ser Asp Pro Gln Leu Ile Val Gln Leu Arg Phe Cys Gly Arg
65 70 75 80
Gln Pro Cys Gly Arg Phe Leu Arg Ala Tyr Arg Glu Gly Ala Leu Arg
85 90 95
Ala Ala Leu Gln Arg Ser Leu Ala Ala Ala Leu Ala Gln His Ser Val
100 105 110
Pro Leu Gln Leu Glu Leu Arg Ala Gly Ala Glu Arg Leu Asp Ala Leu
115 120 125
Leu Ala Asp Glu Glu Arg Cys Leu Ser Cys Ile Leu Ala Gln Gln Pro
130 135 140
Asp Arg Leu Arg Asp Glu Glu Leu Ala Glu Leu Glu Asp Ala Leu Arg
145 150 155
Asn Leu Lys Cys Gly Ser Gly Ala Arg Gly Gly Asp Gly Glu Val Ala
160 165 170 175
Ser Ala Pro Leu Gln Pro Pro Val Pro Ser Leu Ser Glu Val Lys Pro
180 185 190
Pro Pro Val Pro Pro Pro Ala Gln Thr Phe Leu Phe Gln Gly Gln Pro
195 200 205
Val Val Asn Arg Pro Leu Ser Leu Lys Asp Gln Gln Thr Phe Ala Arg
210 215 220

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Ser Val Gly Leu Lys Trp Arg Lys Val Gly Arg Ser Leu Gln Arg Gly
225 230 235 240
Cys Arg Ala Leu Arg Asp Pro Ala Leu Asp Ser Leu Ala Tyr Glu Tyr
245 250 255
Glu Arg Glu Gly Leu Tyr Glu Gln Ala Phe Gln Leu Leu Arg Arg Phe
260 265 270
Val Gln Ala Glu Gly Arg Arg Ala Thr Leu Gln Arg Leu Val Glu Ala
275 280 285
Leu Glu Glu Asn Glu Leu Thr Ser Leu Ala Glu Asp Leu Leu Gly Leu
290 295 300
Thr Asp Pro Asn Gly Glu Leu Ala
305 310

<210> 187
<211> 600
<212> DNA
<213> Homo sapiens

<400> 187
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ctggtggaag gactggctct tcagtagctt taccaggaag gaattttgac agaaaaccac 120
attcaagaaa tcaaagctca aaccacaggc ctccgggaaga caatgctgtt gctggacatc 180
ctgccttcca ggggcccaca agcttttgac accttctcg attccctcca ggaatttccc 240
tgggtaagag agaagctgga gaaggcgaga gaggaagctc cagccgagct gcctacaggt 300
gactgtagtg ccggaatccc ctacacatc ctacagcagt cgccatcaga ccagcagatt 360
aaccagctgg atcagaagct aggcccgagg tgggagcccg tggctcgtgc tctggagctg 420
tccacagcgg acatctaccg ctgcaaggcc aaccatcccc acaacgtgca ttcgaggtg 480
gtggaggcct ttgtccgctg gcgccagcgt ttgggaagc aggccacctt cctaagctta 540
cacaaggcgc tccaggcagt ggaggctgat ccctccctgc tccagcacat gctggagtga 600

<210> 188
<211> 199
<212> PRT
<213> Homo sapiens

<400> 188
Met Glu Ala Arg Asp Lys Gln Val Leu Arg Ser Leu Arg Leu Glu Leu
1 5 10 15
Gly Ala Glu Val Leu Val Glu Gly Leu Val Leu Gln Tyr Leu Tyr Gln
20 25 30
Glu Gly Ile Leu Thr Glu Asn His Ile Gln Glu Ile Lys Ala Gln Thr
35 40 45
Thr Gly Leu Arg Lys Thr Met Leu Leu Leu Asp Ile Leu Pro Ser Arg
50 55 60
Gly Pro Lys Ala Phe Asp Thr Phe Leu Asp Ser Leu Gln Glu Phe Pro
65 70 75 80
Trp Val Arg Glu Lys Leu Glu Lys Ala Arg Glu Glu Val Thr Ala Glu
85 90 95
Leu Pro Thr Gly Asp Trp Met Ala Gly Ile Pro Ser His Ile Leu Ser
100 105 110
Ser Ser Pro Ser Asp Gln Gln Ile Asn Gln Leu Ala Gln Lys Leu Gly
115 120 125
Pro Glu Trp Glu Pro Val Val Leu Ser Leu Gly Leu Ser Gln Thr Asp
130 135 140
Ile Tyr Arg Cys Lys Ala Asn His Pro His Asn Val His Ser Gln Val
145 150 155
Val Glu Ala Phe Val Arg Trp Arg Gln Arg Phe Gly Lys Gln Ala Thr
160 165 170
Phe Leu Ser Leu His Lys Gly Leu Gln Ala Val Glu Ala Asp Pro Ser
175 180 185 190
Leu Leu Gln His Met Leu Glu
195

<210> 189
<211> 1642
<212> DNA

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PT/US2003/024918

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<213> Homo sapiens

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cgcgtgcaga agctctctcg cgagctgctg atgctgtgctg agcagaacga cctggagccc 300
gggacacacg agctcgaggg gggggcgctg gccctccctgc ggcgccacga cctgctgcgg 360
cgcgtcgarg acttcgaggg gggggcgctg ggcctggggc cgcctgggga agaagacctg 420
tgtgcagcat ttaacgtcat atgtgataat gtggggaagc attggagaag attggagagc 480
cagctcaaa gtcacgacac caagatcgac agcatcgagg acagataccc ccgcgaacct 540
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gtggccacc tgggtggggc tctcaggctc tgcagatga gggccatgtc ccgatgtca 720
caagagtttc agcaggcccg tgacctccag aacaggagtg gggccatgtc ccgatgtca 780
tggaactcag acgcatctac ctccgaagcg tcctgatggg ccgctgcttt gcgctgtgtg 840
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aggttgaaga ctggagcttg agctgggac actatgggca aaaggatggt ttgtcccatc tcttggagg 1260
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aggattatgg gtctctgcaa ggcagcggga tctctgtatc ttaaaaagca gtcctcttat 1620
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<210> 190

<211> 208

<212> PRT

<213> Homo sapiens

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<400> 190
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20 25 30
Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met
35 40 45
Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg
50 55 60
Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg Val Asp
65 70 75
Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly Glu Glu Asp
85 90 95
Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly Lys Asp Trp
100 105 110
Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys Ile Asp Ser
115 120 125
Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val Arg Glu Ser
130 135 140
Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr Val Ala His
145 150 155
Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala Asp Leu
165 170 175
Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg Ser Gly Ala
180 185 190
Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser Glu Ala Ser
195 200 205
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<210> 191

<211> 3492

<212> DNA

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49076.000004pct2 1.0.207.655 Seq List Text 07.24.03.txt
<213> Homo sapiens

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<400> 191
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ggctcccgct gactctctga cagggtggaa gactcgagg gactcgagg acagaaaccg 240
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gatgcagctc gacgtccac atccc aacac cctgtgtggca ccccgaggaa tgcagactgt 480
ccccagccag tgtccacag cctctctgct tctcagttgg actga tigtgt ggtgtgacag ccccgagcag 540
ccaagcactc cttctctgct tctcagttgg actga tigtgt ggtgtgacag ccccgagcag 540
gactctgctc actgtgtgat cgtgtcagat agggcccggg gtacacaggg ccccgagcag 540
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gtttctgccc acattggacc cactctggg catatgagc agactgctgc gactggcag 3240
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gtcgaaaaaa aa

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<210> 192
<211> 425
<212> PRT
<213> Homo sapiens

<400> 192

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PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
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 Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr
 20 25 30
 Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr
 35 40 45
 Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys
 50 55 60
 Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg
 65 70 75 80
 Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu
 85 90 95
 Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly
 100 105 110
 Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys
 115 120 125
 Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg
 130 135 140
 Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met
 145 150 155 160
 Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly
 165 170 175
 Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln
 180 185 190
 Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro
 195 200 205
 Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu
 210 215 220
 Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile
 225 230 235 240
 Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys Lys Lys Pro Leu
 245 250 255
 Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro Ala Asp Lys Ala
 260 265 270
 Arg Gly Thr Gln Gly Pro Glu Gln His Leu Leu Ile Thr Ala Pro
 275 280 285
 Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg
 290 295 300
 Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser
 305 310 315 320
 Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro
 325 330 335
 Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile Val Asn Val Cys
 340 345 350
 Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr
 355 360 365
 Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln
 370 375 380
 Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu Thr
 385 390 395 400
 Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly
 405 410 415
 Val Pro Asp Ala Gly Met Lys Pro Ser
 420 425

<210> 193
 <211> 1799
 <212> DNA
 <213> Homo sapiens

<400> 193
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 aatacaccca cgtatgccga tctactttaa gggctgaaac ccacgggcct gagagactat 120
 aagagcgttc cctaccgaca tggaaacaac gggacagaac gcccgcggcg cttcgggggc 180
 ccggaagaag ccagggccag gaccaggaga ggcgcgggga gccaggcgct ggctccgggt 240
 ccccaagacc ctgtgtctgc ttgtcgcggc ggtctgtctg ttggtctcag ctgagctctgc 300
 tctgatcacc caacaagacc tagctcccca cgagagagcg gccccaacac aaaagaggtc 360
 cagccctca gagggattgt gtcacacttg acaccatatt tcagaagacg gttagagattg 420

http://www.uspto.gov/patent

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 gaagtgccgc acaggggtgt cagaggggagt ggtcaagggtc ggtgattgta caccctggag 660
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 agtcttgatt cgtgctgtgt ttgtttgcaa gtctttactg tggagaagaa tccttctcta 780
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<210> 194
 <211> 411
 <212> PRT
 <213> Homo sapiens

<400> 194
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 20 25 30
 Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
 35 40 45
 Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
 50 55 60
 Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
 65 70 75
 Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
 80 85 90
 Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Phe
 100 105 110
 Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
 115 120 125
 Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Gly Thr Phe
 130 135 140
 Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys
 145 150 155
 Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile
 160 165 170
 Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala
 175 180 185
 Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp
 190 195 200
 Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly
 205 210 215
 Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp
 220 225 230
 Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro
 235 240 245
 Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn
 250 255 260
 Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala
 265 270 275
 Glu Arg Ser Gln Arg Arg Glu Leu Val Pro Ala Asn Glu Gly Asp
 280 285 290
 Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val

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305 310 315 320
Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp
325 330 335
Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr
340 345 350
Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala
355 360 365
Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu
370 375 380
Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met
385 390 395 400
Tyr Leu Glu Gly Asn Ala Asp Ser Ala Leu Ser
405 410

<210> 195
<211> 683
<212> DNA
<213> Homo sapiens

<400> 195
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ctcttcagag gtgtctgttt ctgtccttgt ggcaatagct ttggggcttc tgactgcagt 180
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tgggtctcaa gccccaagct gtgaagttcc ttacactgg gtgtgtaaga aggtcagact 600
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gctggccact ggctgttggg aaa 683

<210> 196
<211> 189
<212> PRT
<213> Homo sapiens

<400> 196
Met Thr Asp Ser Val Ile Tyr Ser Met Leu Glu Leu Pro Thr Ala Thr
1 5 10 15
Gln Ala Gln Asn Asp Tyr Gly Pro Gln Lys Ser Ser Ser Arg
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Pro Ser Cys Ser Cys Leu Val Ala Ile Ala Leu Gly Leu Leu Thr Ala
35 40 45
Val Leu Leu Ser Val Leu Leu Tyr Gln Trp Ile Leu Cys Gln Gly Ser
50 55 60
Asn Tyr Ser Thr Cys Ala Ser Cys Pro Ser Cys Pro Asp Arg Trp Met
65 70 75 80
Lys Tyr Gly Asn His Cys Tyr Tyr Phe Ser Val Glu Glu Lys Asp Trp
85 90 95
Asn Ser Ser Leu Glu Phe Cys Leu Ala Arg Asp Ser His Leu Val
100 105 110
Ile Thr Asp Asn Gln Glu Met Ser Leu Leu Gln Val Phe Leu Ser Glu
115 120 125
Ala Phe Cys Trp Ile Gly Leu Arg Asn Asn Ser Gly Trp Arg Trp Glu
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Asp Gly Ser Pro Leu Asn Phe Ser Arg Ile Ser Ser Asn Ser Phe Val
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Gln Thr Cys Gly Ala Ile Asn Lys Asn Gly Leu Gln Ala Ser Ser Cys
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<212> DNA

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<213> Homo sapiens

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<212> PRT
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35 40 45
Ser Ile Met Arg Arg Val Asn His Lys Asp Pro His Val Ala Met Gln
50 55 60
Ala Leu Thr Leu Leu Gly Ala Cys Val Ser Asn Cys Gly Lys Ile Phe

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Leu Asn Lys Gly His Pro Lys Val Cys Glu Lys Leu Lys Ala Leu Met
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Val Glu Trp Thr Asp Glu Phe Lys Asn Asp Pro Gln Leu Ser Leu Ile
      115      120      125
Ser Ala Met Ile Lys Asn Leu Lys Glu Gln Gly Val Thr Phe Pro Ala
      130      135      140
Ile Gly Ser Gln Ala Ala Glu Gln Ala Lys Ala Ser Pro Ala Leu Val
      145      150      155      160
Ala Lys Asp Pro Gly Thr Val Ala Asn Lys Lys Glu Gln Glu Asp Leu
      165      170      175      180
Ala Lys Ala Ile Glu Leu Ser Leu Lys Glu Gln Arg Gln Gln Ser Thr
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Thr Leu Ser Thr Leu Tyr Pro Ser Thr Ser Ser Leu Leu Thr Asn His
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Gln His Glu Gly Arg Lys Val Arg Ala Ile Tyr Asp Phe Glu Ala Ala
      215      220      225
Glu Asp Asn Glu Leu Thr Phe Lys Ala Gly Glu Ile Thr Val Leu
      230      235      240
Asp Asp Ser Asp Pro Asn Trp Trp Lys Gly Glu Thr His Gln Gly Ile
      245      250      255
Gly Leu Phe Pro Ser Asn Phe Val Thr Ala Asp Leu Thr Ala Glu Pro
      260      265      270
Glu Met Ile Lys Thr Glu Lys Lys Thr Val Gln Phe Ser Asp Asp Val
      275      280      285
Gln Val Glu Thr Ile Glu Pro Glu Pro Glu Pro Ala Phe Ile Asp Glu
      290      295      300
Asp Lys Met Asp Gln Leu Leu Gln Met Leu Gln Ser Thr Asp Pro Ser
      305      310      315
Asp Asp Gln Pro Asp Leu Pro Glu Leu Leu His Leu Glu Ala Met Cys
      320      325      330
His Gln Met Gly Pro Leu Ile Asp Glu Lys Leu Glu Asp Ile Asp Arg
      335      340      345
Lys His Ser Glu Leu Ser Glu Leu Asn Val Lys Val Met Glu Ala Leu
      350      355      360
Ser Leu Tyr Thr Lys Leu Met Asn Glu Asp Pro Met Tyr Ser Met Tyr
      365      370      375
Ala Lys Leu Gln Asn Gln Pro Tyr Tyr Met Ser Ser Gly Val Ser
      380      385      390
Gly Ser Gln Val Tyr Ala Gly Pro Pro Pro Ser Gly Ala Tyr Leu Val
      395      400      405
Ala Gly Asn Ala Gln Met Ser His Leu Gln Ser Tyr Ser Leu Pro Pro
      410      415      420
Glu Gln Leu Ser Ser Leu Ser Gln Ala Val Val Pro Pro Ser Ala Asn
      425      430      435
Pro Ala Leu Pro Ser Gln Gln Thr Gln Ala Ala Tyr Pro Asn Thr Met
      440      445      450
Val Ser Ser Val Gln Gly Asn Thr Tyr Pro Ser Gln Ala Pro Val Tyr
      455      460      465
Ser Pro Pro Pro Ala Ala Thr Ala Ala Ala Thr Ala Asp Val Thr
      470      475      480
Leu Tyr Gln Asn Ala Gly Pro Asn Met Pro Gln Val Pro Asn Tyr Asn
      485      490      495
Leu Thr Ser Ser Thr Leu Pro Gln Pro Gly Gly Ser Gln Gln Pro Pro
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Gln Pro Gln Gln Pro Tyr Ser Gln Lys Ala Leu Leu
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 <211> 2531
 <212> DNA
 <213> Homo sapiens

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http://www.uspto.gov/patent

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 <212> PRT
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 35 40 45
 Arg Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val Pro Val Ser Glu
 50 55 60
 Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val Asn Asp Lys
 65 70 75 80
 Val Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp Lys Leu Gly
 85 90 95
 Asp Ser Pro Ile Gln Lys His Lys Gln Tyr Thr Ser Cys Ser Phe
 100 105 110
 Ile Gln Asn Leu Val Ser Ala Ser Leu Gly Ser Thr Ser Lys Asn Thr
 115 120 125
 Ser Pro Met Arg Asn Ser Phe Ala His Ser Leu Ser Pro Thr Leu Glu
 130 135 140
 His Ser Ser Leu Phe Ser Gly Ser Tyr Ser Ser Leu Ser Pro Asn Pro
 145 150 155 160
 Leu Asn Ser Arg Ala Val Glu Asp Ile Ser Ser Ser Arg Thr Asn Pro

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210 215 220
Gly Lys Leu Ser Asn Trp Glu Pro Lys Asp Asp Ala Met Ser Glu His
225 230 235 240
Arg Arg His Phe Pro Asn Cys Pro Phe Leu Glu Asn Ser Leu Gly Thr
245 250 255
Leu Arg Phe Ser Ile Ser Asn Leu Ser Met Gln Thr His Ala Arg
260 265 270
Met Arg Thr Phe Met Tyr Trp Pro Ser Ser Val Pro Val Gln Pro Glu
275 280 285
Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Gly Arg Asn Asp Asp Val
290 295 300
Lys Cys Phe Cys Cys Asp Gly Gly Leu Arg Cys Trp Glu Ser Gly Asp
305 310 315 320
Asp Pro Trp Val Glu His Ala Lys Trp Phe Asp Arg Cys Glu Phe Leu
325 330 335
Ile Arg Met Lys Gly Gln Glu Phe Val Asp Glu Ile Gln Gly Arg Tyr
340 345 350
Pro His Leu Glu Gln Leu Leu Ser Thr Ser Asp Thr Thr Gly Glu
355 360 365
Glu Asn Ala Asp Pro Pro Ile His Phe Gly Pro Gln Ser Ser
370 375 380
Ser Glu Asp Ala Val Met Met Asn Thr Pro Val Val Lys Ser Ala Leu
385 390 395 400
Glu Met Gly Phe Asn Arg Asp Leu Val Lys Gln Thr Val Gln Ser Lys
405 410 415
Ile Leu Thr Thr Gly Glu Asn Tyr Lys Thr Val Asn Asp Ile Val Ser
420 425 430
Ala Leu Leu Asn Ala Glu Asp Glu Lys Arg Glu Glu Glu Lys Glu Lys
435 440 445
Gln Ala Glu Glu Met Ala Ser Asp Asp Leu Ser Leu Ile Arg Lys Asn
450 455 460
Arg Met Ala Leu Phe Gln Gln Leu Thr Cys Val Leu Pro Ile Leu Asp
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Lys Gln Lys Thr Gln Ile Pro Leu Gln Ala Arg Glu Leu Ile Asp Thr
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515 520 525
Lys Glu Ile Asp Ser Thr Leu Tyr Lys Asn Leu Phe Val Asp Lys Asn
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Met Lys Tyr Ile Pro Thr Glu Asp Val Ser Gly Leu Ser Leu Glu Glu
545 550 555 560
Gln Leu Arg Arg Leu Gln Glu Arg Thr Cys Lys Val Cys Met Asp
565 570 575
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<213> Homo sapiens

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35 40 45
Ile Ile Asn Asn Lys Asn Phe His Lys Ser Thr Gly Met Thr Ser Arg
50 55 60
Ser Gly Thr Asp Val Asp Ala Ala Asn Leu Arg Glu Thr Phe Arg Asn
65 70 75 80
Leu Lys Tyr Glu Val Arg Asn Lys Asn Leu Thr Arg Glu Glu Ile
85 90 95
Val Glu Leu Met Arg Asp Val Ser Lys Glu Asp His Ser Lys Arg Ser
100 105 110
Ser Phe Val Cys Val Leu Leu Ser His Gly Glu Glu Gly Ile Ile Phe
115 120 125
Gly Thr Asn Gly Pro Val Asp Leu Lys Lys Ile Thr Asn Phe Phe Arg
130 135 140
Gly Asp Arg Cys Arg Ser Leu Thr Gly Lys Pro Lys Leu Phe Ile Ile
145 150 155
Gln Ala Cys Arg Gly Thr Glu Leu Asp Cys Gly Ile Glu Thr Asp Ser
160 165 170 175
Gly Val Asp Asp Asp Met Ala Cys His Lys Ile Pro Val Glu Ala Asp
180 185 190

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225 240
Arg Lys Val Ala Thr Glu Phe Glu Ser Phe Ser Phe Asp Ala Thr Phe
245 255
His Ala Lys Lys Gln Ile Pro Cys Ile Val Ser Met Leu Thr Lys Glu
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Leu Tyr Phe Tyr His
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<211> 1906

<212> DNA

<213> Homo sapiens

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gaacagaaac agaaaaggc gcggttatct gcttcagaag gagaggaagt tcttcaagac 420
aaggcgccaa gctatgttcc tttcctgcta attggtggag gcacagctgc ttttgcctga 480
gccagatcca gtgcggctcg ggaatcctggg gccagggtac gtattgtatc tgaagatctc 540
gagctgcctg acatgcgacc tctcttttca aaagaactgt ggttttcaga tgaccaccaat 600
gtcacaaga cactgcgatt caaacagtgg aatggaaaag agagaagcat atatttcag 660
ccacctctct tctatgtctc tgcctcaggac ctgcctcata ttgagaattg tgggtggct 720
gtcctcactg ggaagaaggt agtacacgtg gatgtgagag acaacatggt gaaacttaat 780
gagggctctc aaataaccta tgaaaagtgc ttgattgcaa caggagggtac tccaagaagt 840
ctgtctgcga ttgataggcg tggagcagag gtgaagagta gaacaacgtc tttcagaag 900
attggagact ttagaagcct ggagaagatt tcacgggaag tcaaatcaat tacgatattc 960
gggtggggct tctctggtag cgaactggcc tgtgctcttg gcagaaaggc tcgagccttg 1020
ggcacagaag tgattcaact ctcccccgag aaaggaataa tgggaaagat cctccccgaa 1080
tacctcagca acttgaccat ggaaaaaatc agacagagag ggtgttaagt gatgccaat 1140
gctattgtgc aactcgttgg agtcagcagt gcacaagtac tatctcaagc gaagacggc 1200
auggaggtag aaactgacca catagtggca gctgtgggcc tggagcccaa tgttgagtg 1260
gccaaagact gtgcccgtga aatagactca gatitttggt gcttccgggt aaatcgagag 1320
ctacaagcac gctctaacat ctgggtggca ggagatcgtg catgctctta cgatataaag 1380
ttgggaagga ggcgggtaga gcacctgat cacgctgttg tgaagtgaag atttggctga 1440
gaaaataatga ctggagctgc taagccgtac tggcatcagt caatgttctg gagggtattg 1500
ggccccgatg ttggtcatga agctatttgg ctgtgtgaca ctgtgttgcg cactgttgg 1560
gttttttgcaa aagacaactgc acaagacac ccctaatctg ccacagagca gtcaggaact 1620
ggatctgcga cagcagagtga cagagatcc gagggcctag gaagcctcag aaattactat tcttccagc 1680
accccgagca ttccaacagc tcccgctcag ggggaggact acggcaagg tgctactctc 1740
tacctcaggg acaaatgtgt cgtggggatt acatctttaa acgaatgcca 1800
atagcaagga agatcattaa ggaagggtag cagcatgaag attcctaaga agtagccaa 1860
ctattcaaca tcatgaaga ctgaagcccc acagtgaat ttgcaa 1906

<210> 204

<211> 613

<212> PRT

<213> Homo sapiens

<400> 204

Met Phe Arg Cys Gly Leu Ala Ala Gly Ala Leu Lys Gln Lys Leu
1 5 10 15
Val Pro Leu Val Arg Thr Val Cys Val Arg Ser Pro Arg Gln Arg Asn
20 25 30
Arg Leu Pro Gly Asn Leu Phe Gln Arg Trp His Val Pro Leu Glu Leu
35 40 45
Gln Met Thr Arg Gln Met Ala Ser Ser Gly Ala Ser Gly Gly Lys Ile
50 55 60
Asp Asn Ser Val Leu Val Leu Ile Val Gly Leu Ser Thr Val Gly Ala
65 70 75 80

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 Gly Ala Tyr Ala Tyr Lys Thr Met Lys Glu Asp Glu Lys Arg Tyr Asn
 85 90 95
 Glu Arg Ile Ser Gly Leu Gly Leu Thr Pro Glu Gln Lys Gln Lys Lys
 100 105 110
 Ala Ala Leu Ser Ala Ser Glu Gly Glu Val Pro Gln Asp Lys Ala
 115 120 125
 Pro Ser His Val Pro Phe Leu Ile Gly Gly Gly Thr Ala Ala Phe
 130 135 140
 Ala Ala Ala Arg Ser Ile Arg Ala Arg Asp Pro Gly Ala Arg Val Leu
 145 150 155
 Ile Val Ser Glu Asp Pro Glu Leu Pro Tyr Met Arg Pro Pro Leu Ser
 160 165 170 175
 Lys Glu Leu Trp Phe Ser Asp Asp Pro Asn Val Thr Lys Thr Arg
 180 185 190
 Phe Lys Gln Trp Asn Gly Lys Glu Arg Ser Ile Tyr Phe Gln Pro Pro
 195 200 205
 Ser Phe Tyr Val Ser Ala Gln Asp Leu Pro His Ile Glu Asn Gly Gly
 210 215 220
 Val Ala Val Leu Thr Gly Lys Lys Val Val Gln Leu Asp Val Arg Asp
 225 230 235 240
 Asn Met Val Lys Leu Asn Asp Gly Ser Gln Ile Thr Tyr Glu Lys Cys
 245 250 255
 Leu Ile Ala Thr Gly Gly Thr Pro Arg Ser Leu Ser Ala Ile Asp Arg
 260 265 270
 Ala Gly Ala Glu Val Lys Ser Arg Thr Thr Leu Phe Arg Lys Ile Gly
 275 280 285
 Asp Phe Arg Ser Leu Glu Lys Ile Ser Arg Glu Val Lys Ser Ile Thr
 290 295 300
 Ile Ile Gly Gly Gly Phe Leu Gly Ser Glu Leu Ala Cys Ala Leu Gly
 305 310 315 320
 Arg Lys Ala Arg Ala Leu Gly Thr Glu Val Ile Gln Leu Phe Pro Glu
 325 330 335
 Lys Gly Asn Met Gly Lys Ile Leu Pro Glu Tyr Leu Ser Asn Trp Thr
 340 345 350
 Met Glu Lys Val Arg Arg Glu Gly Val Lys Val Met Pro Asn Ala Ile
 355 360 365
 Val Gln Ser Val Gly Val Ser Ser Gly Lys Leu Leu Ile Lys Leu Lys
 370 375 380
 Asp Gly Arg Lys Val Glu Thr Asp His Ile Val Ala Ala Val Gly Leu
 385 390 395 400
 Glu Pro Asn Val Glu Leu Ala Lys Thr Gly Gly Leu Glu Ile Asp Ser
 405 410 415
 Asp Phe Gly Gly Phe Arg Val Asn Ala Glu Leu Gln Ala Arg Ser Asn
 420 425 430
 Ile Trp Val Ala Gly Asp Ala Ala Cys Phe Tyr Asp Ile Lys Leu Gly
 435 440 445
 Arg Arg Arg Val Glu His His Asp His Ala Val Val Ser Gly Arg Leu
 450 455 460
 Ala Gly Glu Asn Met Thr Gly Ala Ala Lys Pro Tyr Trp His Gln Ser
 465 470 475 480
 Met Phe Trp Ser Asp Leu Gly Pro Asp Val Gly Tyr Glu Ala Ile Gly
 485 490 495
 Leu Val Asp Ser Ser Leu Pro Thr Val Gly Val Phe Ala Lys Ala Thr
 500 505 510
 Ala Gln Asp Asn Pro Lys Ser Ala Thr Glu Gln Ser Gly Thr Gly Ile
 515 520 525
 Arg Ser Glu Ser Glu Thr Glu Ser Glu Ala Ser Val Ile Thr Ile Pro
 530 535 540
 Pro Ser Thr Pro Ala Val Pro Gln Ala Pro Val Gln Gly Glu Asp Tyr
 545 550 555 560
 Gly Lys Gly Val Ile Phe Tyr Leu Arg Asp Lys Val Val Val Gly Ile
 565 570 575
 Val Leu Trp Asn Ile Phe Asn Arg Met Pro Ile Ala Arg Lys Ile Ile
 580 585 590
 Lys Asp Gly Glu Gln His Glu Asp Leu Asn Glu Val Ala Leu Phe
 595 600 605
 Asn Ile His Glu Asp
 610

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<210> 205
<211> 1090
<212> DNA
<213> Homo sapiens

<400> 205
atggccgctg acaggggacg caggatattg ggagtggtg gcatgcatcc tcatcatcag 60
gaactcttaa aaaagaaccg agtgggtgcta gccaaacagc tgttgttgag cgaattgtta 120
gaactctctc tggagaaagg catcatcacc ttggaaatga gggagctcat ccaggccaaa 180
gtgggcagtt tcagccagaa tttggaactc ctcaacttgc tgcctaaagag ggttccccaa 240
gcttttgatg cttccttgga agccttgcac tcttgaattt tatcaaacac acttccagct 300
ggcatatagg ttgcagcttc ggctctgtgg cctagcactg gtgttgagca atgtgcactt 360
cactggagag aaagaactgg aatttcgttc tggaggggat gtggaccaca gtactctagt 420
caccctcttc aagcttttgg gctatgacgt ccatgttcta tgtgaccaga ctgcacagga 480
aatgcaagag aaactgcaga attttgcaca gttactctga caccgagtga cgagctctg 540
catctgtgca ctctctctgc atggtgtgga gggcgccatc tatgtgtggt atgggaaact 600
gtctcagctc caagagggttt ttcagctctt tgacaacgcc aaccgcccaa gcctacagaa 660
caaaccaaaa atgttcttca tccagcgctg ccgtggagat gagactaatc gtgggggtga 720
ccaacaagat ggaaagaacc acgcaggatc ccctgggtgc gaggagatgt atggcggtaa 780
agaaaagtgt ccgaagatga gactgccacc gcgctcagac atgatattgc gctatgctg 840
cctcaaaagg actgccacca tgcggaacac caaacgaggt tcttggtaca tcgaggctct 900
tgctcaagtg ttttctgagc gggcttgtga tatgcactgt gccgacatgc tggttaaggt 960
gaacgcactt atcaaggatc gggaaggtaa tgctctggc acagaatttc accggtgcaa 1020
ggagatgtct gaatactgca gcatctctgt ccgccacctc tacctgttcc caggacacct 1080
tcccacatga                                     1090

<210> 206
<211> 91
<212> PRT
<213> Homo sapiens

<400> 206
Met Ala Ala Asp Arg Gly Arg Arg Ile Leu Gly Val Cys Gly Met His
1 5 10 15
Pro His His Gln Glu Thr Leu Lys Lys Asn Arg Val Val Leu Ala Lys
20 25 30
Gln Leu Leu Leu Ser Glu Leu Leu Glu His Leu Leu Glu Lys Asp Ile
35 40 45
Ile Thr Leu Glu Met Arg Glu Leu Ile Gln Ala Lys Val Gly Ser Phe
50 55 60
Ser Gln Asn Val Glu Leu Leu Asn Leu Leu Pro Lys Arg Gly Pro Gln
65 70 75 80
Ala Phe Asp Ala Phe Cys Glu Ala Leu His Ser
85 90

<210> 207
<211> 714
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion polynucleotide

<400> 207
tctgatcagg agcccaaatc ttgtgacaaa actcacacat gccacacgtg ccagcacct 60
gaactctctg ggggaccgtc agtcttcttc ttccccccaa aaccacaagg accctctatg 120
atctcccgga cccctgaggt cacatgcgtg gtgggtgacg tgagccacga agacctgtag 180
gtcaagtcca actgtgtact ggacggcggt gaggtgcata atgccaaagc aaagccggg 240
gaggagcagt acaaacgacg gtaccgtgtg tctcagcttc ctaccgtctc gcaccaggac 300
tggctgtaag gcaaggagta caagtgtcaag gtctccaaca aagccctccc agccccctac 360
gagaaaaaaa tcttcaaaag caaagggcag ccccgagaga cacagtgtta cactctgccc 420
catcccgagg atgagctgac caagaaccag gtccagccta cctgctctgt caaagctctc 480
tatccacagg acatgcgcgt ggagtgggag agcaatgggc agcggagaaa caactacaag 540
accacgcctc ccgtgtctga ctccgacggc tctcttcttc tctacagcaa gctcacctgt 600
gacaaagaca ggtgtcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 660
cacaaccact acacgcagaa gagcctcttc ctgtctccgg gtaaatgacg taga 714

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<210> 208
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion polypeptide

<400> 208
Ser Asp Gln Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
1 5 10 15
Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
20 25 30
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
35 40 45
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
50 55 60
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
65 70 75 80
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
85 90 95
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
100 105 110
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
115 120 125
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Ser Arg Asp
130 135 140
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
145 150 155 160
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
165 170 175
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
180 185 190
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
195 200 205
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
210 215 220
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
225 230 235

<210> 209
<211> 718
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion polynucleotide

<221> misc_feature
<222> 34, 43, 52, 55, 58, 64
<223> n = A,T,C or G

<400> 209
tgatcaagaa ccacatggag gatgcacgtg ccncagtgcc ccncaatgcc cngcncnnga 60
actncaagga ggccctctcg tctttgtctt ccccccgaaa cccaaggacg tcctctcccat 120
ttttggaggc cgagtcacgt gcgttgtagt ggcagctcga aagaagagacc ccgaggtcaa 180
tttcaactgg tatattgatg gcgttgaggt ggcgaacggc caaagagga 240
acagttcaac agcagctacc gcgtgggtcag cgtctgccc atccagcacc aggactggct 300
gacggggaag gaattcaagt gcaagggtcaa caaaaagct ctcccggccc ccactcgagag 360
gacctctccc aaggccaaag ggcagaccgc ggagccgcag gtgtacaccc tggcccacaa 420
ccgggaagaa ctggccaagg acaccgtagc cgtaacatgc ctggtcaaa gcttctaccc 480
agctgacatc aacgttgagt ggcagaggaa cggtcagccg gagtcagagg gcacctacgc 540
caacacgcgc ccacagctgg acaacgacgc gacctacttc ctctacagca agctctcggt 600
gggaaagaac acgtggcagc ggggagaaac cttaacctgt gtggtgatgc atgaggccct 660
gcacaaccac tacaccaga aatccatcac ccagctctcg ggtaaatagt aatctaga 718

<210> 210
<211> 757

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<212> DNA

<213> Artificial Sequence

<220>

<223> Fusion polynucleotide

<400> 210

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tgtatcaagaa cccaagacac caaaaccaca accacaacca caaccacaaac ccaatcctac 60
aacagaatcc aagtgtccca aatgtccagc ccctgagctc ctgggagggc cctcagtcct 120
catcttcccc ccgaaaccca aggagctcct ctccatttct gggaggcccg aggtcacgtg 180
cgctgtggta gacgtgggcc aggaagaccc cgaggtcagt ttcaactggt acattgatgg 240
cgctgaggtg cgaacggcca acacagagcc aaaagaggaa cagtccaaca gcacgtaccg 300
cgctgtcagc gtcttgcca tccagaccca ggactggctg acgggggaagg aattcaagtg 360
caaggtcaac aacaaagctc tcccggccc catcgagaag accatctcca aggccaaagg 420
cgagaccggg gagccgagg tgtaaccctt ggcccacac cgggaaggag cgttgagtg 480
caccgtgagc gtaacatgcc tgggtcaagg ctctaccca ctgatatac acgttgagtg 540
cgagaggaaat gggcagcggg agtcagaggg cacytacgcc accagccac cccagctgga 600
caacgacggg acctacttcc tctacagcaa gctctcggtg ggaagaacac cgtggcagca 660
gggagaagacc ttacactgtg tgggtgatga cgaggccctg cacaaccact acaccagaa 720
attcatcacc cagtcttcgg gtaaatagta atctaga
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<210> 211

<211> 727

<212> DNA

<213> Artificial Sequence

<220>

<223> Fusion polynucleotide

<400> 211

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tgtatcaagc caccacagcg aagaccgccg ctccaagtgt cccaatgcc caggccctga 60
actccttgga gggccacagc tcttcatctt cccccgaaa gccaaaggag tctctccat 120
cacccgaaaaa cctgaggtca cgtgcttggt gtggagctgg gtaaaagaa cctcgagatc 180
gagttcaagc tgggtcgtgg atgacacaga ggtacacacg gctgagacaa agccaaagga 240
ggaacagttc aacagcagct accgcgtggt cagcttcttg ccatccagc accaggactg 300
gctgacgggg aaggaaattca agtgcaaggt caacaacaaa gctctccag ccccatcaga 360
gaggaccatc tccaaggcca aagggcagac cgggagccg caggtgtaca cctgtggccc 420
acaccgggaa gagctggcca aggacacggt gagcgtaacc tgcttggtca aaggcttctt 480
cccagctgac atcaacggtt agtggcagag gaatgggcag ccggagtcag agggcaccta 540
cgccaacacg ccgcacacag tggacaacga cgggaccctac ttctctaca gcaaacctctc 600
cgtgggaaag aacacgtggc agcagggaga agtcttccac tgtgtgtga tgacagggc 660
tctacacaaat cactccacc agaaatccat caccagctt tcgggtaaat agtaactctag 720
agggccc
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<210> 212

<211> 231

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion polypeptide

<400> 212

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Glu Pro His Gly Gly Cys Thr Cys Pro Gln Cys Pro Ala Pro Glu Leu
1 5 10 15
Pro Gly Gly Pro Ser Val Phe Val Phe Pro Pro Lys Pro Lys Asp Val
20 25 30
Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val Asp Val
35 40 45
Gly Lys Glu Asp Pro Glu Val Asn Phe Asn Trp Tyr Ile Asp Gly Val
50 55 60
Glu Val Arg Thr Ala Asn Thr Lys Pro Lys Glu Glu Gln Phe Asn Ser
65 70 75 80
Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp Trp Leu
85 90 95
Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ala
100 105 110
Pro Ile Glu Arg Thr Ile Ser Lys Ala Lys Gly Gln Thr Arg Glu Pro
115 120 125
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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu Leu Ala Lys Asp Thr
 130 135 140
 Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Ala Asp Ile Asn
 145 150 155 160
 Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr Tyr Ala
 165 170 175
 Asn Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu Tyr Ser
 180 185 190
 Arg Leu Ser Val Gly Lys Asn Thr Trp Gln Arg Gly Glu Thr Leu Thr
 195 200 205
 Gly Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 210 215 220
 Ile Thr Gln Ser Ser Gly Lys
 225 230

<210> 213
 <211> 248
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fusion polypeptide

<400> 213
 Asp Gln Glu Pro Lys Thr Pro Lys Pro Gln Pro Gln Pro Gln
 1 10 15
 Pro Asn Pro Thr Thr Glu Ser Lys Cys Pro Lys Cys Pro Ala Pro Glu
 20 25 30
 Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp
 35 40 45
 Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val Val Asp
 50 55 60
 Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile Asp Gly
 65 70 75 80
 Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln Phe Asn
 85 90 95
 Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp Trp
 100 105 110
 Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro
 115 120 125
 Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr Arg Glu
 130 135 140
 Pro Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu Leu Ala Lys Asp
 145 150 155 160
 Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro Asp Ile
 165 170 175
 Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr Tyr
 180 185 190
 Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu Tyr
 195 200 205
 Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Gln Gly Glu Thr Phe
 210 215 220
 Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 225 230 235 240
 Ser Ile Thr Gln Ser Ser Gly Lys
 245

<210> 214
 <211> 236
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fusion polypeptide

<400> 214
 Asp Gln Ala His His Ser Glu Asp Pro Ser Ser Lys Cys Pro Lys Cys

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 1 5 10 15
 Pro Gly Pro Glu Leu Leu Gly Gly Pro Thr Val Phe Ile Phe Pro Pro
 20 25 30
 Lys Ala Lys Asp Val Leu Ser Ile Thr Arg Lys Pro Glu Val Thr Cys
 35 40 45
 Leu Trp Trp Thr Trp Val Lys Thr Leu Arg Ser Ser Ser Ser Trp
 50 55 60
 Ser Val Asp Asp Thr Glu Val His Thr Ala Glu Thr Lys Pro Lys Glu
 65 70 75
 Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln
 80 85 90
 His Gln Asp Trp Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn
 95 100 105
 Lys Ala Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Ala Lys Gly
 110 115 120
 Gln Thr Arg Glu Pro Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu
 125 130 135
 Leu Ala Lys Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Phe
 140 145 150
 Pro Ala Asp Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser
 155 160 165
 Glu Gly Thr Tyr Ala Asn Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr
 170 175 180
 Tyr Phe Leu Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Gln
 185 190 195
 Gly Glu Val Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His
 200 205 210
 Ser Thr Gln Lys Ser Ile Thr Gln Ser Ser Gly Lys
 215 220 225
 230 235

<210> 215

<211> 54

<212> DNA

<213> Artificial sequence

<220>

<223> Fusion polynucleotide

<400> 215

gatcaggagc ccaaatcttg tgacaaaact cacacatgcc caccggtgcc agca 54

<210> 216

<211> 18

<212> PRT

<213> Artificial sequence

<220>

<223> Fusion polypeptide

<400> 216

Asp Gln Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 1 5 10 15
 Pro Ala

<210> 217

<211> 54

<212> DNA

<213> Artificial sequence

<220>

<223> Fusion polynucleotide

<400> 217

gatctggagc ccaaatcttg tgacaaaact cacacatgcc caccggtgcc agca 54

<210> 218

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion polypeptide

<400> 218
Asp Leu Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
1 5 10 15
Pro Ala

<210> 219
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion polynucleotide

<400> 219
cctgaactcc tggggggacc gtcagttctc ctcttccccc caaaacccaa ggacaccctc 60
atgatctccc ggacccttga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct 120
gaggtcaagt tcaacttgta cgtggacggc gtggaggtgc ataaagccaa gacaaagccg 180
cgggaggagc agtacaacag cagtcaccgt gtggtcagcg tcttcaccgt cctgcaccag 240
gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cccagccccc 300
atcgagaaaa ccattctcaa agccaaa 327

<210> 220
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion polypeptide

<400> 220
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
1 5 10 15
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
20 25 30
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
35 40 45
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
50 55 60
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
65 70 75 80
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
85 90 95
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
100 105

<210> 221
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion polynucleotide

<400> 221
gggcagctcc gagaaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag 60
aaccaagttca gcttgaccty ccttggtcaaa ggcttctatc ccagcgacat cgcctggag 120
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcttcccggt gctggactcc 180
gacggctctt tcttctctta tagcaagctc accgtggaca agagcaggtg gcagcagggg 240
aacgtcttct catgctccgt gatgcatgag gctctgcaca accattacac gcagaagagc 300

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt 324

<210> 222
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion polypeptide

<400> 222
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
1 5 10 15
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
20 25 30
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45
Asn Asn Tyr Ser Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 223
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion polynucleotide

<400> 223
gatcaggagc ccaatcttc tgacaaaact cacacatccc caccgtcccc agca 54

<210> 224
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion polypeptide

<400> 224
Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser
1 5 10 15
Pro Ala

<210> 225
<211> 712
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion polynucleotide

<400> 225
tgatcacccc aaatcttctg acaaaactca cacatctcca cgtcctcag cactgaact 60
ctcgggtgga cgtcagttc tcctcttccc cccaaaacc aaggacacc tcattgatctc 120
cggaccctt gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgagggtcaa 180
gttcaactgg tacgtggacg gcgtggaggt gcataatgcc aagacaagc cgcgggagga 240

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gcagtagaac agcacgtacc gtgtgggtcag cgtctctacc gtcttcgacc aggactggct 300
gaatggcaag gagtacaagt gcaaggtctc caacaaagcc ctccagcccc ccactggagaa 360
aacaattctcc aaagccaaag ggcagccccc agaaccacag gtgtacaccc tgcccccatc 420
ccgggatgag ctgaccaaga accaggtcag cctgacctgc ctggtcaaat gcttctatcc 480
cagcgacatc gccgtggagt gggagagcaa tgggcagccg gagaacaact acagaccac 540
gcttcccggtg ctggactccg acggtctctt ctctctctac agcaagctca ccgtggacaa 600
gagcaggtgg cagcagggga acgtctctc atgctccgtg atgcatgagg cctgcacaa 660
ccactacacg cagaagagcc tctcctgtc tccgggtaaa tgataatcta ga 712

<210> 226
<211> 233
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion polypeptide

<400> 226
Asp His Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Ser
1 5 10 15
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
20 25 30
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
35 40 45
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
50 55 60
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
65 70 75 80
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
85 90 95
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
100 105 110
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
115 120 125
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
130 135 140
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
145 150 155
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
160 165 170
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Leu
175 180 185
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
190 195 200
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
205 210 215 220
Lys Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 227
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' primer for llama IgG1 constant region

<400> 227
gttgttgatc aagaaccaca tggaggatgc acgtg

35

<210> 228
<211> 32
<212> DNA
<213> Artificial Sequence

<220>

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
<223> 5' primer for llama ig2 constant region

<400> 228
gtgtgtgac aagaacccaa gacacaaaa cc 32

<210> 229
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' primer for llama IgG3 constant region

<400> 229
gtgtgtgac aagcgacca cagcgaagac ccc 33

<210> 230
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Llama Fc sense sequencing primer

<400> 230
ctgagatcga gtccagctg 19

<210> 231
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Llama Fc antisense sequencing primer

<400> 231
cctcctttgg ctttgtctc 19

<210> 232
<211> 1527
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<221> misc_feature
<222> 843, 852, 861, 864, 867, 873
<223> n = A,T,C or G

<400> 232
aagcttgccg ccatggattt tcaagtgcag attttcagct tcctgctaatt cagtgtctca 60
gtcataattg ccagaggaca aattgtcttc tccagctctc cagcaatcct gtctgcatct 120
ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg 180
taccagcaga agccaggatc ctccccaaa cctctggattt atgcccctac caacctggct 240
tcctggattcc ctgctcgctt cagtggcagt gggctcggga cctcttactc tctcaaatc 300
agcagagtgg aggcctgaaga tgcctccact tattactgcc agcagttggag ttttaaccaca 360
ccacagctcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcgggtggt 420
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggtg 480
agggcctgggg ctctcagtga gatgtcctgc aaggcctctg gctacacatt taccagttac 540
aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600
ccaggaaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660
gacaaatcct ccagcacagc ctacatgcag ctcagcagc tgacatctga agactctgctg 720
gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cagtgtctgg 780
ggcacaggga ccacggctac cgtctctctt gatcaagaac cacatggagg atgcacgtgc 840

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 gcagtgcgaa aagaagacc cagaggtcaat ttcaactgggt atattgatgg cgttgagggtg 1020
 cgaagggcca atacgaagcc aaaagaggaa cagttcaaca gcacgtaccg cgttgtcagc 1080
 gtctcgccc tccagaccac ggaactggctg acggggaagg aattcaagtg caaggtcaac 1140
 aacaagaagctc tcccgcccc catcgagagg accattccca aggcacaagg gcagaccgg 1200
 gagcgcaggg tgtacacctt gggcccacac cgggaagaac cgtgacatca acggtgagtg 1260
 gtaacatgctc tgttcaaaag ctctaccaca cacttacggc aacacgcgcg gcagcgtgag 1320
 ggtcagcgcg agtcagaggg gctcagcagg cactacgtgg gaaaagaaca cgtggcagcg 1380
 acctactctc ttgtgatgca tgaggcctgt ggaacacact acaccagaa atccatcacc 1440
 ttaacctgtg tgggtgatga tgaggcctgt ggaacacact acaccagaa atccatcacc 1500
 cagctctcgg gtaaatagta atctaga ggaacacact acaccagaa atccatcacc 1527

<210> 233
 <211> 1566
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion polynucleotide

<400> 233
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 gtcataattg ccagaggaca aattgtcttc tccagctctc cagcaatcct gctgtcatct 120
 ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaaagta catgcatcgg 180
 taccagcaga agccaggatc ctcccccaaa ccttggaatt atgcccacat caactctggct 240
 tctggagctc ctgctgcctt cagtggcagt gggctcggga ctcttactc tctcaaatc 300
 agcagagtg aggtcgaaga tgcctgccat tattaactgc agcagtgagg ttttaaccca 360
 cccacgttgc gtgctgggac caagctggag cgtgtggctc gcggtggctc gggcgtgggt 420
 ggaactggag gagggtggag ctctcaggct tatctacagc agtctggggc tgagctgtgt 480
 aggcctgggg ctctagtgaa gatgtctctg aaggctcttg gctacacatt taccagttac 540
 aatatgcact gggtaaagca gacacctaga caggcctcgg aatggattgg agctatttat 600
 ccaggaaatg gtataacttc ctacaatcag aagttcaagg agtgcactgt agtactgta 660
 gacaattcct ccagcacagc ctacatgcag ctacagcagc tgacattctga agactctcgg 720
 gtctaatctt gtccaagagt ggtgtactat agtaactctt actgttactt cgtatcttgg 780
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 cctgagctcc tggggaggcc ctacagctctc atctctcccc cgaaccccaa ggacgtcttc 960
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 gaggtcagtt tcaacttgta cattgatggc gtgtgtcagc tctgtcccat cagcagcag 1080
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 gcccacacc gggaagagct gcgcaaggac acctgagcg taacatgctt gttcaacca 1320
 ttctaccacc ctgatataca cgttgagtg cagaagaatg ggcagccgga gtcagagg 1380
 acytaccca ccaagccacc ccagctggac aacgacggga ctaactctct ctacagcaga 1440
 ctctcgggtg gaagaacac gtggcagcag ggagaaacct tcaacttgtt ggtgatgac 1500
 gaggccctgc acaaccacta caccagaaa tccatcacc agtctcggg taaatagtaa 1566
 tctaga

<210> 234
 <211> 1536
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion polynucleotide

<400> 234
 aagcttgccg ccatggattt tcaagtgcag attttcagct tcctgctaatt cagtgtctca 60
 gtcataattg ccagaggaca aattgtcttc tccagctctc cagcaatcct gctgtcatct 120
 ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaaagta catgcatcgg 180
 taccagcaga agccaggatc ctcccccaaa ccttggaatt atgcccacat caactctggct 240
 tctggagctc ctgctgcctt cagtggcagt gggctcggga ctcttactc tctcaaatc 300
 agcagagtg aggtcgaaga tgcctgccat tattaactgc agcagtgagg ttttaaccca 360
 cccacgttgc gtgctgggac caagctggag ctctcaggct tatctacagc gcggtggctc gggcgtgggt 420
 ggtcagcgag gagggtggag ctctcaggct tatctacagc agtctggggc tgagctgtgt 480
 aggcctgggg ctctagtgaa gatgtcctgc aaggctcttg gctacacatt taccagttac 540
 aatatgcact gggtaaagca gacacctaga aatggattgg agctatttat 600

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 gtctatttct gtgcaagagt ggtgtactat agtaactctt actgtgtactt cgtgtctgg 780
 ggcaagagga ccacggtcac cgtctcttct gatcaagcga accacagcga agacccagc 840
 tccaagtgtc ccaaatgccg aggccctgaa ctcttggag ggccacggt ctctatcttc 900
 cccccgaag ccaaggacgt cctctccatc acccgaaaac ctgaggctac gtgcttgg 960
 tggacgtggg taaagaagac cctgagatcg agttcaagct ggtcgtgga tgacacagag 1020
 gtacacacgg ctgagacaaa gccaaaaggag gaacagtcca acagcacgta ccgctgggtc 1080
 agcgtctctgc cctccagca ccaggactgg ctgacgggga aggaattcaa gtgcaaggct 1140
 aacaacaaag ctctccagc cccatcgag aggcactct ccaaggccaa agggcagacc 1200
 cgggagccgc aggtgtcac cctggcccca cccgggaag agctggccaa ggacaccgtg 1260
 agcgttaact agctgttcaa aggtctcttc ccagctgaca tcaactgtga gtggcagagg 1320
 aatgggcagc cggagtcaga gggcactcac gccaacagc gcgcacagct ggacaacgac 1380
 gggactctat tctctacag caaactcttc gtgggaaga acacgtggca gcagggagaa 1440
 gtcttcacct gtgtgtgat gcacgaggct ctacacaatc actccacca gaaatccatc 1500
 accagctctt cgggtaata gtaatctaga gggccc 1536

<210> 235
 <211> 498
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 235
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro His Gly
 260 265 270
 Gly Cys Thr Cys Pro Gln Cys Pro Ala Pro Glu Leu Pro Gly Gly Pro
 275 280 285
 Ser Val Phe Val Phe Pro Pro Lys Asp Val Leu Ser Ile Phe
 290 295 300
 Gly Gly Arg Val Thr Cys Val Val Val Asp Val Gly Lys Lys Asp Pro
 305 310 315 320
 Glu Val Asn Phe Asn Trp Tyr Ile Asp Gly Val Glu Val Arg Thr Ala
 325 330 335
 Asn Thr Lys Pro Lys Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 340 345 350
 Ser Val Leu Pro Ile Gln His Gln Asp Trp Leu Thr Gly Lys Glu Phe
 355 360 365
 Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ala Pro Ile Glu Arg Thr
 370 375 380
 Ile Ser Lys Ala Lys Gly Gln Thr Arg Glu Pro Gln Val Tyr Thr Leu
 385 390 400
 Ala Pro His Arg Glu Glu Leu Ala Lys Asp Thr Val Ser Val Thr Cys
 405 410 415
 Leu Val Lys Gly Phe Tyr Pro Ala Asp Ile Asn Val Glu Trp Gln Arg
 420 425 430
 Asn Gly Gln Pro Glu Ser Glu Gly Thr Tyr Ala Asn Thr Pro Pro Gln
 435 440 445
 Leu Asp Asn Asp Gly Thr Tyr Phe Leu Tyr Ser Lys Leu Ser Val Gly
 450 455 460
 Lys Asn Thr Trp Gln Arg Gly Glu Thr Leu Thr Cys Val Val Met His
 465 470 475 480
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Ile Thr Gln Ser Ser
 485 490 495
 Gly Lys

<210> 236

<211> 514

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 236

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Thr
 260 265 270
 Pro Lys Pro Gln Pro Gln Pro Gln Pro Asn Pro Thr Thr Glu
 275 280 285
 Ser Lys Cys Pro Lys Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

290 295 300

Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Ser Ile Ser Gly
305 310 315 320

Arg Pro Glu Val Thr Cys Val Val Val Asp Val Gly Gln Glu Asp Pro
325 330 335

Glu Val Ser Phe Asn Trp Tyr Ile Asp Gly Ala Glu Val Arg Thr Ala
340 345 350

Asn Thr Arg Pro Lys Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val
355 360 365

Ser Val Leu Pro Ile Gln His Gln Asp Trp Leu Thr Gly Lys Glu Phe
370 375 380

Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
385 390 395 400

Ile Ser Lys Ala Lys Gly Gln Thr Arg Glu Pro Gln Val Tyr Thr Leu
405 410 415

Ala Pro His Arg Glu Glu Leu Ala Lys Asp Thr Val Ser Val Thr Cys
420 425 430

Leu Val Lys Gly Phe Tyr Pro Pro Asp Ile Asn Val Glu Trp Gln Arg
435 440 445

Asn Gly Gln Pro Glu Ser Glu Gly Thr Tyr Ala Thr Thr Pro Pro Gln
450 455 460

Leu Asp Asn Asp Gly Thr Tyr Phe Leu Tyr Ser Lys Leu Ser Val Gly
465 470 475 480

Lys Asn Thr Trp Gln Gln Gly Glu Thr Phe Thr Cys Val Val Met His
485 490 495

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Ile Thr Gln Ser Ser
500 505 510

Gly Lys

<210> 237
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 237

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15

Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30

Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45

Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60

Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95

Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110

Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125

Asp Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser
130 135 140

Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145 150 155 160

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165 170 175

Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
210 215 220

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

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 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Ala His Ser His
 260 270
 Ser Glu Asp Pro Ser Ser Lys Cys Pro Lys Cys Pro Gly Pro Glu Leu
 275 280 285
 Leu Gly Gly Pro Thr Val Phe Ile Phe Pro Pro Lys Ala Lys Asp Val
 290 295 300
 Leu Ser Ile Thr Arg Lys Pro Glu Val Thr Cys Leu Trp Trp Thr Trp
 305 310 315 320
 Val Lys Lys Thr Leu Arg Ser Ser Ser Ser Trp Ser Val Asp Asp Thr
 325 330 335
 Glu Val His Thr Ala Glu Thr Lys Pro Lys Glu Glu Gln Phe Asn Ser
 340 345 350
 Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp Trp Leu
 355 360 365
 Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ala
 370 375 380
 Pro Ile Glu Arg Thr Ile Ser Lys Ala Lys Gly Gln Thr Arg Glu Pro
 385 390 395 400
 Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu Leu Ala Lys Asp Thr
 405 410 415
 Val Ser Val Thr Cys Leu Val Lys Gly Phe Phe Pro Ala Asp Ile Asn
 420 425 430
 Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr Tyr Ala
 435 440 445
 Asn Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu Tyr Ser
 450 455 460
 Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Gln Gly Glu Val Phe Thr
 465 470 475 480
 Cys Val Val Met His Glu Ala Leu His Asn His Ser Thr Gln Lys Ser
 485 490 495
 Ile Thr Gln Ser Ser Gly Lys
 500

<210> 238

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> 3'-primer for llama IgG1, IgG2, IgG3 constant region

<400> 238

gtgttttcta gattactatt taccgaaga ctgggtgatg ga

42

<210> 239

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 239

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 gtcataattg ccaggaggaca aattgttctc tccagctctc cagcaatcct gtctgcatct 120
 ccaggggaga aggtcacaat gacttgcagg gccagctcaa gtgtaagtta catgactctg 180
 taccagcaga agccaggatc ctcccccaaa cctctgattt atgccccatc caacctggct 240
 tctggagttc ctgctgcctt cagtggcagt gggctggga cctcttactc tctcacaatc 300
 agcagagtgg aggcctaaga tgcctgcact tattactgcc agcagtggag ttttaacca 360
 cccacgttgc gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtgg 420
 ggaactggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggt 480
 aggcctgggg cctcagtgaa gatgtctctg aaggctctcg gctacacatt taccagttac 540
 aatatgcact gggtaaaaca gacacctaga cagggcctcg aatggattgg agctatttat 600
 ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660

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ggcacaggga ccacggtcac cgtctcttct gatcaggagc ccaaatcttg tgacaaaact 840
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ccccaaaac ccaaggacac cctcatgac tcctcgacc ctgaggtcac atgctgtgtg 960
gtggacgtga gccacgaaga ccttgaggtc aagtccaact ggtacgtgga cggcgtggag 1020
gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtgttc 1080
agcgtctctca cgtctctgca ccaggactgg ctgaatggca aggagtagaa gtgcaaggtc 1140
tccacaaaag cctctccagc cccatcgag aaaacaatct ccaaagccaa agggcagccc 1200
cgagaaccac aggtgttacac cctgccccc tcccggtgat agctgaccaa gaaccaggtc 1260
agcctgacct gccctgtcaa aggtctctat cccagcgaca tcgctgtgga gtgggagagc 1320
aatggggcagc cggagaaacaa ctacaagacc acgctctccc tgcgtgagtc cgacggcttc 1380
ttctctctctc acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgcttc 1440
tcacgtctcg tgatgcagga ggctctgcac aaccactaca cgcagaagag cctctctctg 1500
tctccgggta aatgactag a 1521

<210> 240

<211> 500

<212> PRT

<213> Artificial sequence

<220>

<223> fusion polypeptide

<400> 240

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125
Asp Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser Ser
130 135 140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145 150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165 170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
210 215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225 230 235 240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245 250 255
Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser
260 265 270
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
275 280 285
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
290 295 300
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
305 310 315 320
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
325 330 335
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
340 345 350

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
355 360 365
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Asp Pro Ala Pro
370 375 380
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
385 390 395 400
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
405 415
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
420 430
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
435 440 445
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
450 455 460
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
465 470 475 480
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
485 490 495
Ser Pro Gly Lys
500

<210> 241
<211> 162
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 241
gcgagtcctt cgaacctgct cccatctcgg gccattacct taatctcagt aaatggaatt 60
tttgatgat gctgcctgac ctactgcttt gccccaagat gcagagagag aaggaggaat 120
gagagattga gaaggggaag tgtacgccct gtataatcgt at 162

<210> 242
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 242
Ala Asp Pro Ser Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser
1 5 10 15
Val Asn Gly Ile Phe Val Ile Cys Lys Leu Thr Tyr Cys Phe Ala Pro
20 25 30
Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val
35 40 45
Arg Pro Val
50

<210> 243
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 243
aagcttatgg attttcaagt gcagattttc agcttctcgc taatcagtc ttcagtcata 60
atgtccagag gagtgcagat tgttctgact cagtctccag ccacctgtc tgtgactcca 120
ggagatagag ttctcttttc ctgcagggcc agccaagta ttacgacta cttaactgg 180
ttcaacaaca aatcacatga gtctccaagg ctctcatca aatatgtctc ccattccatc 240
tctgggatcc ctctcagggt cagtggcagt ggcacagggt cagatttcac tctcagatc 300
aacagtgtgg aacctgaaga tgttggaaat tattactgtc aacatgggtc cagctttccg 360

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
tggacgttcg gtggaggcac caagctggaa atcaaacgg 399

<210> 244
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 244
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Ala
20 25 30
Thr Leu Ser Val Thr Pro Gly Asp Arg Val Ser Leu Ser Cys Arg Ala
35 40 45
Ser Gln Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln Gln Lys Ser His
50 55 60
Glu Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser His Ser Ile Ser Gly
65 70 75
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Phe Thr Leu
80 85 90
Ser Ile Asn Ser Val Glu Pro Glu Asp Val Gly Ile Tyr Tyr Cys Gln
100 105 110
His Gly His Ser Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu
115 120 125
Ile Lys Arg
130

<210> 245
<211> 368
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 245
cagatccagt tgggtgcaatc tggacctgag ctgaagaagc ctggagagac agtcaggatc 60
tcctgcaagg ctctgggta tgccttcaca actactggaa tgcagtgggt gcaagagatg 120
caggaaaggt gtttgaagt gattggctgg ataaacacc cactctggag tgccaaata 180
tgtagaagac ttcaaggacg gtttgccttc tctttggaaa cctctgccaa cactgcata 240
ttacagataa gcaacctcaa agatgaggac acggctacgt attctgtgt gagatccggg 300
aatgttaact atgacctggc ctactttgct tactggggcc aagggacact ggtcactgtc 360
tctgatca 368

<210> 246
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 246
Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
1 5 10 15
Thr Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Thr Thr
20 25 30
Gly Met Gln Trp Val Gln Glu Met Pro Gly Lys Gly Leu Lys Trp Ile
35 40 45
Gly Trp Ile Asn Thr Pro Leu Trp Ser Ala Lys Ile Cys Arg Arg Leu
50 55 60
Gln Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Asn Thr Ala Tyr
65 70 75
Leu Gln Ile Ser Asn Leu Lys Asp Glu Asp Thr Ala Thr Tyr Phe Cys
80 85 90 95

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Val Arg Ser Gly Asn Gly Asn Tyr Asp Leu Ala Tyr Phe Ala Tyr Trp
100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser
115 120

<210> 247
<211> 812
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 247
aagcttatgg attttcaagt gcagattttc agcttcctgc taatcagtcg ttcagtcata 60
atgtccagag gagtgcacat tgttctgact cagtctccag ccacctgtc tgtgactcca 120
ggagatagag tctctctttc ctgcagggcc agccagagta ttacgcacta cttacactgg 180
tatcaacaaa aatcacatga gtctcccaagg ctctcatca aatatgtctc ccattccatc 240
tctgggattcc cctccaggtt cagtggcagt ggatcagggt cagatttcac tctcagtatc 300
aacagtgtgg aacctgaaga tgttggaaatt tattactgtc aacatgtcca cagctttccc 360
tggagcttctg gtggaggcac caagctggaa atcaaacggg gtggcggtgg ctggggcgga 420
gggtgggtcgg gtggcggtgg atctcagatc cagttgtgtc aatctggacc tgagctgaag 480
aagcttggag agacagtcag gatctctctg aaggcttctg ggatgcctt cacaactact 540
ggaatgcagt ggggtgcaaga gatgccagga aagggtttga agtggattgg ctggataaac 600
accctactct ggagtgccaa aatatgtaga agacttcaag gacgggtttg ctctctcttg 660
gaaacctctg ccaacactgc atattacag ataagcaacc tcaaagatga ggacacggct 720
acgtatttct gtgtgagatc cgggaatggt aactatgacc tggcctactt tgcttactgg 780
ggccaaggga cactggtcac tgtctctgat ca 812

<210> 248
<211> 267
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 248
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Ala
20 25 30
Thr Leu Ser Val Thr Pro Gly Asp Arg Val Ser Leu Ser Cys Arg Ala
35 40 45
Ser Gln Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln Gln Lys Ser His
50 55 60
Glu Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser His Ser Ile Ser Gly
65 70 75 80
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Phe Thr Leu
85 90 95
Ser Ile Asn Ser Val Glu Pro Glu Asp Val Gly Ile Tyr Tyr Cys Gln
100 105 110
His Gly His Ser Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu
115 120 125
Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140
Gly Ser Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro
145 150 155 160
Gly Glu Thr Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr
165 170 175
Thr Thr Gly Met Gln Trp Val Gln Glu Met Pro Gly Lys Gly Leu Lys
180 185 190
Trp Ile Gly Trp Ile Asn Thr Pro Leu Trp Ser Ala Lys Ile Cys Arg
195 200 205
Arg Leu Gln Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Asn Thr
210 215 220
Ala Tyr Leu Gln Ile Ser Asn Leu Lys Asp Gly Asp Thr Ala Thr Tyr
225 230 235 240

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Phe Cys Val Arg Ser Gly Asn Gly Asn Tyr Asp Leu Ala Tyr Phe Ala
245 250 255
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
260 265

<210> 249
<211> 405
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 249
atggattttc aagtgcagat tttagcttc ctgctaata ctgcttcagt cataatgtcc 60
agaggagtcg acattgtgct caccacatct ccagcttctt tggctgtgct tctaggtcag 120
agagccacca tctcttgtag agccagtga aagtgtgaat attatgtcac aagtttaagt 180
cagtggtacc aacagaaacc aggcagacca ccaaaactcc tcattctctg tgcattcaac 240
gtagaatctg ggggtccctg caggtttagt ggcagtgagg ctgggacaga cttcagcttc 300
aacatccatc ctgtggagga ggaatgatatt gcaatgtatt tctgtcagca aagtaggaag 360
gttctctgga cgttcgggtg aggcaccaag ctggaaatca aatcg 405

<210> 250
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 250
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Ala
20 25 30
Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala
35 40 45
Ser Gln Ser Val Gln Tyr Tyr Val Thr Ser Leu Met Gln Trp Tyr Gln
50 55 60
Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Ser Ala Ala Ser Asn
65 70 75
Val Gln Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
80 85 90 95
Asp Phe Ser Leu Asn Ile His Pro Val Gln Gln Asp Asp Ile Ala Met
100 105 110
Tyr Phe Cys Gln Gln Ser Arg Lys Val Pro Trp Thr Phe Gly Gly Gly
115 120 125
Thr Lys Leu Gln Ile Lys Arg
130 135

<210> 251
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 251
cagggtgcagc tgaaggagtc aggcactggc ctggtggcgc cctcacagag cctgtccatc 60
acatgcaccg tctcagggtt ctcatcaacc ggctatgggt taaactgggt tcgccagcct 120
caggaaagggt gctcggagtg gctgggaatg atatgggggt atggaagcac agactataat 180
tcagctctca aatccagact gagcatcacc aaggacacct ccaagagcca agtttctta 240
aaaatgaaca gtcgtcaaac tgatgacaca gccagatact actgtgccag agatggttat 300
agtaactttc attactatgt tatggactac tggggctcaag gaacctcagt caccgtctcc 360
tcagatctgt

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<210> 252
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 252
Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln
1 5 10 15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Gly Tyr
20 25 30
Gly Val Asn Trp Val Arg Gln Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45
Gly Met Ile Trp Gly Asp Gly Ser Thr Asp Tyr Asn Ser Ala Leu Lys
50 55 60
Ser Arg Leu Ser Ile Thr Lys Asp Asn Ser Lys Ser Gln Val Phe Leu
65 70 75
Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala
85 90 95
Arg Asp Gly Tyr Ser Asn Phe His Tyr Tyr Val Met Asp Tyr Trp Gly
100 105 110
Gln Gly Thr Ser Val Thr Val Ser
115 120

<210> 253
<211> 825
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 253
aagcttatgg attttcaagt gcagattttc agcttctctgc taatcagtcg ttcagtcata 60
atgtccagag gagtcgacat tgtgtctacc caatctccag cttctttggc tgtgtctcta 120
ggtcagagag ccaccatctc ctgcagagcc agtgaagtg ttgaatatta tgtcacaagt 180
ttaatgtagt ggtaccaaca gaaaccagga cagccaccca aactctctcat ctctgtgcca 240
tccaagctag aatctggggg cctgtgccagg tttagtgcca gtgggtctgg gacagacttc 300
agcctcaaca tccatcttgt ggaggagat gatatgcaa tgtattctgt tcagcaaaagt 360
aggaagggttc cttggacgtt cgggtgagcg accaagctgg aatatcaacg ggggtggcgt 420
ggctcgggcg gaggtgggtc ggggtggcgc ggatctcagg tgcagctgaa ggagtcagga 480
cctgtccttg tggcgccctc acagagcctg tccatcacat gcacgtcttc aggggtctca 540
ttaaccggct atgggtgtaa ctgggttctc cagcctccag gaaagggtct ggagtggctg 600
ggaatgatat ggggtgatgg aagcacagac tataattcag ctctcaaatc cagactgagc 660
atcaccaggg acaactccaa gagccaagtt ttcttaaaaa tgaacagctc gcaaacgtgat 720
gcacacagcca gatactactg tggccagagt gggtatagta acttccatta ctatgttatg 780
gactactggg gtcaaggaac ctccagtcacc gtctcctctg atcag 825

<210> 254
<211> 271
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 254
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Ala
20 25 30
Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala
35 40 45
Ser Glu Ser Val Glu Tyr Tyr Val Thr Ser Leu Met Gln Trp Tyr Gln
50 55 60
Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Ser Ala Ala Ser Asn

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
65 Val Glu Ser Gly Val⁷⁰ Pro Ala Arg Phe⁷⁵ Ser Gly Ser Gly Ser Gly Thr⁸⁰
85
Asp Phe Ser Leu Asn Ile His Pro Val⁹⁰ Glu Glu Asp Asp Ile Ala Met⁹⁵
100
Tyr Phe Cys Gln Gln Ser Arg Lys Val¹⁰⁵ Pro Trp Thr Phe Gly Gly Gly¹¹⁰
115
Thr Lys Leu Glu Ile Lys Arg Gly Gly Gly Ser Gly Gly Gly¹²⁵
130
Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Lys¹³⁵ Glu Ser Gly Pro Gly¹⁴⁰
145
Leu Val Ala Pro Ser¹⁵⁰ Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly¹⁶⁰
165
Phe Ser Leu Thr Gly Tyr Gly Val Asn¹⁷⁰ Trp Val Arg Gln Pro Pro Gly¹⁷⁵
180
Lys Gly Leu Glu Trp Leu Gly Met Ile Trp Gly Asp Gly Ser Thr Asp¹⁸⁵
190
Tyr Asn Ser Ala Leu Lys Ser Arg Leu Ser Ile Thr Lys Asp Asn Ser¹⁹⁵
200
Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Thr Thr Asp Asp Thr²⁰⁵
210
Ala Arg Tyr Tyr Cys²¹⁵ Ala Arg Asp Gly Tyr Ser Asn Phe His Tyr Tyr²²⁰
225
Val Met Asp Tyr²³⁰ Trp Gly Gln Gly Thr²³⁵ Ser Val Thr Val Ser Ser²⁴⁰
245
250
255
260
265
270

<210> 255

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 255

atggattttc aagtgcagat ttccagcttc ctgctaatac gtgcttcagt cataatgtcc 60
agaggagtcg acatccagat gacacagctc ccattctcac tgtctgcatc tctgggaggc 120
aaagtcacca tcacttgcaa ggcaagccaa gacattaaga agtatatagg ttggtaccac 180
cacaagcctg gaaaaggtcc caggctgctc atatattaca catctacatt acagccaggc 240
atcccatcaa ggttcagtcg aactgggttc gggagagatt attccctcag catcagaaac 300
ctggagcctg aagatatatg aactatttat tgtcaacagt atgataattc tccattgacg 360
ttcggtctcg ggacaaagt ggaaataaaa cgg 393

<210> 256

<211> 131

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 256

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5
Val Ile Met Ser Arg Gly Val Asp Ile Gln Met Thr Gln Ser Pro Ser
20 25 30
Ser Leu Ser Ala Ser Leu Gly Gly Lys Val Thr Ile Thr Cys Lys Ala
35 40 45
Ser Gln Asp Ile Lys Lys Tyr Ile Gly Trp Tyr Gln His Lys Pro Gly
50 55 60
Lys Gly Pro Arg Leu Leu Ile Tyr Tyr Thr Ser Thr Leu Gln Pro Gly
65 70 75 80
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Leu
85 90 95
Ser Ile Arg Asn Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln
100 105 110
Gln Tyr Asp Asn Leu Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu
115 120 125

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Ile Lys Arg
130

<210> 257
<211> 362
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 257
gatgtacagc ttcaggagtc aggacgtggc ctgctgaacc ctctcagtc tctgtctctc 60
acctgctctg tcatctggcta ctccatcacc agtggtttct actggaactg gatccgacag 120
tttccgggaa acaaaactgga atggatgggc cacataagcc acgacggtag gaataactac 180
aacccatctc tcataaatcg aatctccatc actcgtgaca catctaagaa ccagtttttc 240
ctgaagtiga gttctgtgac tactgaggac acagctacat atttctgtgc aagacactac 300
ggtagtagcg gagctatgga ctactggggt caaggaaact cagtcaccgt ctctctctgat 360
ca 362

<210> 258
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 258
Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Gly
20 25 30
Phe Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45
Met Gly His Ile Ser His Asp Gly Arg Asn Asn Tyr Asn Pro Ser Leu
50 55 60
Ile Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65 70 75 80
Leu Lys Leu Ser Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys
85 90 95
Ala Arg His Tyr Gly Ser Ser Gly Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110
Thr Ser Val Thr Val Ser Ser
115

<210> 259
<211> 806
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 259
aagcttatgg attttcaagt gcagattttc agcttctctg taatcagtc ttcagtcata 60
atgtccagag gatcgacat ccagatgaca cagtcctcat cctcactgic tgcactctctg 120
ggaggcaaaag tcacatcac ttgcaaggca agccaagaca ttaagaagta tataagtttg 180
taccacacaa agcctggaaa aggtcccagg ctgctcatat attacacatc tacattacag 240
caggcatcc catcaaggtt cagtggaaat gggctctggg gagattatc cctcagcatc 300
agaaaactgg agcctgaaga tattgcaact tattattgtc aacagtatga taatcttcca 360
tgacgcttgc gctcggggac aaagtgtgaa ataaaaacgg gtggcggtgg ctggggcggt 420
ggggggctgg gtggcgcggc atctgatgta cagcttcagg agtcaggacc tggcctctgt 480
aaactctctc agtctctgtc tctcactctg tctgtcactg gctactccat caccagtggt 540
tctcactgga actggatccg acagtttccg ggaacacaa tcggaatggat gggccacata 600
agccacgacg gtaggataaa ctacaacca tctctcataa atcgaattct catcactcgt 660
gacacatcta agaaccagtt tttctcgaag ttgagttctg tgactactga ggacacagct 720

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
acatatttct gtgaagaca ctacgtagt agcggagcta tggactactg gggtaagga 780
acctcagtcac cgcgtctctc tgatca 806

<210> 260
<211> 266
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 260
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Val Asp Ile Gln Met Thr Gln Ser Pro Ser
20 25 30
Ser Leu Ser Ala Ser Leu Gly Gly Lys Val Thr Ile Thr Cys Lys Ala
35 40 45
Ser Gln Asp Ile Lys Lys Tyr Ile Gly Trp Tyr Gln His Lys Pro Gly
50 55 60
Lys Gly Pro Arg Leu Leu Ile Tyr Tyr Thr Ser Thr Leu Gln Pro Gly
65 70 75 80
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Leu
85 90 95
Ser Ile Arg Asn Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln
100 105 110
Gln Tyr Asp Asn Leu Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu
115 120 125
Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
130 135 140
Gly Ser Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro
145 150 155 160
Ser Gln Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr
165 170 175
Ser Gly Phe Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu
180 185 190
Glu Trp Met Gly His Ile Ser His Asp Gly Arg Asn Asn Tyr Asn Pro
195 200 205
Ser Leu Ile Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln
210 215 220
Phe Phe Leu Lys Leu Ser Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr
225 230 235 240
Phe Cys Ala Arg His Tyr Gly Ser Ser Gly Ala Met Asp Tyr Trp Gly
245 250 255
Gln Gly Thr Ser Val Thr Val Ser Ser Asp
260 265

<210> 261
<211> 417
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 261
atggcatgga gctgcattat tttcttcttg gtatcagtaa ttacaggtgt ccattcccgag 60
gtcaagctgc agcagctcgg ttctgaacta gggaaacctg ggcctcagtg gaaactgtcc 120
tgcaagactc caggctacat attcacagat cactatatatt ctggggtgaa acagaagcct 180
ggagaaagcc tgcaagtggat aggaatgttt tatgggtgaa atggtgtgtac aagctacaat 240
caaaaattcc agggcgaaggc cacactgact gtatgataaaa tctctagcac agcctacatg 300
gaactcagca gcctgacatc tgaggattct gcatctatt actgtgcaag aaggccggtg 360
gcgacgggac atgctatgga ctactggggt caggggatcc aagtattcgt ctctcca 417

<210> 262
<211> 139
<212> PRT
<213> Artificial Sequence

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<220>

<223> fusion polypeptide

<400> 262

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Met Ala Trp Ser Cys Ile Ile Phe Phe Leu Val Ser Val Ile Thr Gly
 1      5      10      15
Val His Ser Gln Val Lys Leu Gln Gln Ser Gly Ser Glu Leu Gly Lys
 20      25      30
Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Thr Ser Gly Tyr Ile Phe
 35      40      45
Thr Asp His Tyr Ile Ser Trp Val Lys Gln Lys Pro Gly Glu Ser Leu
 50      55      60
Gln Trp Ile Gly Asn Val Tyr Gly Gly Asn Gly Gly Thr Ser Tyr Asn
 65      70      75      80
Gln Lys Phe Gln Gly Lys Ala Thr Leu Thr Val Asp Lys Ile Ser Ser
 85      90      95
Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile
100      105      110
Tyr Tyr Cys Ala Arg Arg Pro Val Ala Thr Gly His Ala Met Asp Tyr
115      120      125
Trp Gly Gln Gly Ile Gln Val Thr Val Ser Ser
130      135
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<210> 263

<211> 381

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 263

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atgttgatata catctcagct ccttgggctt ttactctctt ggatttcagc ctccagaagt 60
gacatagtgc tgactcagac tccagccact ctgtctcttaa ttccctggaga aagagtcaca 120
atgacctgtca agaccagtca gaatatattggc acaatctttac actggtatca ccaaaaacca 180
aaggaggcttc caagggtctt catcaagtat gcttcgcagt ccatctctgg gatccctccc 240
agattcagtg gcagtggttc ggaacacagat ttcaacttca gcatcaataa cctggagcct 300
gatgatctcg gaatttatta ctgtcaacaa agtagaagct ggcctgtcac gttcggctct 360
ggcaccaagc tggagataaa a
```

<210> 264

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 264

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Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser
 1      5      10      15
Ala Ser Arg Ser Asp Ile Val Leu Thr Gln Thr Pro Ala Thr Leu Ser
 20      25      30
Leu Ile Pro Gly Glu Arg Val Thr Met Thr Cys Lys Thr Ser Gln Asn
 35      40      45
Ile Gly Thr Ile Leu His Trp Tyr His Gln Lys Pro Lys Glu Ala Pro
 50      55      60
Arg Ala Leu Ile Lys Tyr Ala Ser Gln Ser Ile Pro Gly Ile Pro Ser
 65      70      75      80
Arg Phe Ser Gly Ser Gly Ser Glu Thr Asp Phe Thr Leu Ser Ile Asn
 85      90      95
Asn Leu Glu Pro Asp Asp Ile Gly Ile Tyr Tyr Cys Gln Gln Ser Arg
100      105      110
Ser Trp Pro Val Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys
115      120      125
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<210> 265
<211> 1671
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 265
aagcttatgg attttcaagt gcagattttc agcttctcgc taatcagtg ttcagtcata 60
atgtccagag gagtgcagat tgttctgact cagtctccag ccacctgtgc tgtgactcca 120
ggagatagag tctctcttcc ctgcagggcc agccagagta tttagcgacta ctacacatgg 180
tctcaacaaa aatcacatga gtctccaagg ctctctatca aatatgtctc ccattccattc 240
tctgggatcc cctccagggt cagtggcagt ggatcagggt cagatttcac ttcagttatc 300
aacagtgtag aacctgaaga ttttggaatt tattactgtc aacatgggtc cagcttcccg 360
tggacgttct gtggaggcac caagctggaa atcaaacggg gtggcggtgg ctggggcgga 420
gggtgggtcgg gtggcgggcg atctcagatc cagtgtgtgc aatctggacc tgagctgaa 480
aagcctggag agacagtcag gatctcctgc aaggcttctg ggatgtcctt cacaactact 540
ggaaatgcagt ggggtgcaaga gatgccagga aagggtttga agtgatttgg ctggataaac 600
acccctactc ggagtgccaa aatatgtaga agacttcaag gacggtttgc ctctcttttg 660
gaaacctctg ccaacactgc atattttacag ataagcaacc tcaaaagatga ggacacgctc 720
acgtatttct gtgtgagatc cgggaatgggt aactatgacc tggcctactt tgcttactgg 780
ggccaaaggga cctgtgtcac acttggaaact ctggagccca aatcttctga caaaactcac 840
acatcccccac cgtctccagg catgattctc ttgacccctg aggtcacatg cgtggtgggtg 960
ccaaaaccca agacacacct agaggtcaag ctgaactgtt acgtggagcgg ctggagggtg 1020
gcagctgagcc acgaagaccg cgggaggagg cagtacaaca gcacgtaccg tgtgtgtcagc 1080
cataatgcc aagacaaggcc ggactggcgt aatggcaagg agtacaagtg caaggtcttc 1140
gtcttcaccg tcttcgacca gactgcagaa accatttcca aagccaaagg gcagccctga 1200
aacaaagccc tcccagcccc gaaccacagg tgtaacacct gccccatctc cgggatgagc tgaccaagaa ccaagtcagc 1260
ctgacctggc tggtaaaagg ctctcatccc agcgacatcg ccgtggagtg ggagagcaat 1320
ggggcagccg agaacacaat caagaccacg cctcccggtc tggactccga cggctctctc 1380
ttctcttaca gcaagctcac cgtggagcag agcaggtggc agcaggggaa cgtctcttca 1440
tgctccgtga tgcattgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1500
ccgggtgaaag cggatctcttc gaacctgtct ccatctcgtt ccatctcgtt aatctcagta 1560
aatggaattt ttgtgatatg ctgcctgacc tactgtcttt cccaagatg cacagagaga 1620
aggagaatg agagatttag aagggaagt gtacgccttg tataaatcga t 1671

<210> 266
<211> 552
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 266
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Ala
20 25 30
Thr Leu Ser Val Thr Pro Gly Asp Arg Val Ser Leu Ser Cys Arg Ala
35 40 45
Ser Gln Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln Gln Lys Ser His
50 55 60
Glu Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser His Ser Ile Ser Gly
65 70 75 80
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Phe Thr Leu
85 90 95
Ser Ile Asn Ser Val Glu Pro Glu Asp Val Gly Ile Tyr Tyr Cys Gln
100 105 110
His Gly His Ser Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu
115 120 125
Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140
Gly Ser Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro
145 150 155 160
Gly Glu Thr Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr
165 170 175

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 Thr Thr Gly Met Gln Trp Val Gln Met Pro Gly Lys Gly Leu Lys
 180 185 190
 Trp Ile Gly Trp Ile Asn Thr Pro Leu Trp Ser Ala Lys Ile Cys Arg
 195 200 205
 Arg Leu Gln Gly Arg Phe Ala Ser Leu Glu Thr Ser Ala Asn Thr
 210 215 220
 Ala Tyr Leu Gln Ile Ser Asn Leu Lys Asp Glu Asp Thr Ala Thr Tyr
 225 230 235 240
 Phe Cys Val Arg Ser Gly Asn Gly Asn Tyr Asp Leu Ala Tyr Phe Ala
 245 250 255 260
 Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Asp Leu Glu Pro Lys
 260 265 270 275
 Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu
 275 280 285 290
 Leu Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 290 295 300 305
 Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 305 310 315 320
 Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
 325 330 335 340
 Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
 340 345 350 355
 Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 355 360 365 370
 Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
 370 375 380 385
 Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 385 390 395 400
 Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
 400 405 410 415
 Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 415 420 425 430
 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 435 440 445 450
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 450 455 460 465
 Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 465 470 475 480
 Val Met His Glu Ala Leu His Asn His Thr Gln Lys Ser Leu Ser
 480 485 490 495
 Leu Ser Pro Gly Lys Ala Asp Pro Ser Asn Leu Leu Pro Ser Trp Ala
 500 505 510 515
 Ile Thr Leu Ile Ser Val Asn Gly Ile Phe Val Ile Cys Cys Leu Thr
 515 520 525 530
 Tyr Cys Phe Ala Pro Arg Cys Arg Glu Arg Arg Asn Glu Arg Leu
 530 535 540 545
 Arg Arg Glu Ser Val Arg Pro Val
 545 550

<210> 267
 <211> 1683
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion polynucleotide

<400> 267
 aagcttatgg attttcaagt gcagattttc agcttctctgc taatcagtgcc ttcagtcata 60
 atgtccagag gagtcgacat tgtgtctcacc caatctccag ctctcttggc tgtgtctcta 120
 ggtcagagag ccaccatctc ctgcagagcc agtgaaagtg ttgaatttta tgcacaga 180
 tcaatgcagt ggtaccaca gaaaccagga cagccaccga aactcctcat ctctgctga 240
 tccaaagtta aatctggggg ccttccaggg ttatgtggca gtgggtctgg gacagacttc 300
 agcctcaaca tccatctcgt gaggaggagt gatattgcga tgtatttctg tcagcaaatg 360
 aggaaggttc ctgtgacgtt gggtggaggg accaagctgg aatcaaacg ggggtggcgt 420
 ggtctggggc gagggtgggt cgggtggcgg ggaatcagag tgcagctgaa ggaatcagga 480
 ccttggcctg tggcgccttc acagagcctg tccatccat gcacctctc aggttctcta 540
 ttaaccgctg atggtgtaaa ctggttctgc cagcctccag gaaagggtct ggagtggtct 600

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 ggaatgatg ggggtgatg aagcacagac tataattcag ctctcaaatc cagactgagc 660
 ataccacaag acaactccaa gagccaagtt ttcttaaaaa tgaacacgtc gcaactgatg 720
 gacacagcca gatactactg tgccagagat ggttatagta actttcatta ctatgttatg 780
 gactactggg gtaacaggaa ctcagtcacc gtctcctcag atctggagcc caaatcttct 840
 gacaaaactc cccacatccc accgtcccca gcaactgaac tcctgggggg tcctgcagtc 900
 tgcgttggtg tgcataatgc caaggacacc ctcagtgatc cccggacccc tgaggtcaca 960
 ggctggaggg tgcataatgc caacgaagac cctgaggtca agttcaactg gtacgtggac 1020
 cgtgttggtc gcgtctctac cgcgcgaagc ccgctggagg agcagtcaca cagcagctac 1080
 tgcacaagtt ccaacaagac cctccagccc cctcctgagc tgaatggcaa ggagtcagaa 1140
 gggcagcccc gagaaaccaca ggtgtacacc ctgccccatc aaacatctgc caaagccaaa 1200
 aaccaggtca gcttcagctg cctgttcaaa gctcttctatc ccgagtcaga cgtgaccaa 1260
 tgggagagca atgggcagcc ggagaaacac tacaagacca cgctccctgt gctgagctcc 1320
 gacggctcct tcttctctca cagcaagctc accgtggaca agagcagggt cgcagagggg 1380
 aacgtctctt catgtccctg gatgcatgag gctctgcaca accactacac gcagaagagc 1440
 ctctccctgt ctcggggtaa agcggatcct tcgaacctgc tcccatcctg gccattacc 1500
 ttaattctag taatgggaat ttttgtgata tgctgcctga cctactgctt tgcccaaga 1560
 gaagaggaga gaaggaggaa tgaagagatt agaagggaaa gtgtacgcc tgataaatc 1620
 gat 1680

<210> 268
 <211> 556
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 268
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Ala
 20 25 30
 Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala
 35 40 45
 Ser Gln Ser Val Glu Tyr Tyr Val Thr Ser Leu Met Gln Trp Tyr Gln
 50 55 60
 Gln Lys Pro Gly Gln Pro Lys Leu Leu Ile Ser Ala Ala Ser Asn
 65 70 75 80
 Val Gln Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Thr
 85 90 95
 Asp Phe Ser Leu Asn Ile His Pro Val Gln Glu Asp Asp Ile Ala Met
 100 105 110
 Tyr Phe Cys Gln Gln Ser Arg Lys Val Pro Trp Thr Phe Gly Gly Gly
 115 120 125
 Thr Lys Leu Glu Ile Lys Arg Gly Gly Gly Ser Gly Gly Gly Gly
 130 135 140
 Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Lys Glu Ser Gly Pro Gly
 145 150 155 160
 Leu Val Ala Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly
 165 170 175
 Phe Ser Leu Thr Gly Tyr Gly Val Asn Trp Val Arg Gln Pro Gly
 180 185 190
 Lys Gly Leu Glu Trp Leu Gly Met Ile Trp Gly Asp Gly Ser Thr Asp
 195 200 205
 Tyr Asn Ser Ala Leu Lys Ser Arg Leu Ser Ile Thr Lys Asp Asn Ser
 210 215 220
 Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr
 225 230 235 240
 Ala Arg Tyr Tyr Cys Ala Arg Asp Gly Tyr Ser Asn Phe His Tyr Tyr
 245 250 255
 Val Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp
 260 265 270
 Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro
 275 280 285
 Ala Pro Glu Leu Leu Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys
 290 295 300
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 305 310 315 320

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Tyr Tyr
325 330 335
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
340 345 350
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
355 360 365
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
370 375 380
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
385 390 395 400
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
405 410 415
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
420 425 430
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
435 440 445
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
450 455 460
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
465 470 475 480
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
485 490 495
Lys Ser Leu Ser Leu Ser Pro Gly Lys Ala Asp Pro Ser Asn Leu Leu
500 505 510
Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly Ile Phe Val Ile
515 520 525
Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg Glu Arg Arg Arg
530 535 540
Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
545 550 555

<210> 269
<211> 1665
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 269
aagcttatgg attttcaagt gcagattttc agcttcctgc taatcagtcg ttcagtcata 60
atgtccagag gagtgcacat ccagatgaca cagtctccat cctcagctgc tgcattctcg 120
ggaggcaag tcacatcac agccaagaca agccaagaca ttaagaagta tatagctgg 180
taccacaaca agcctggaaa aggtcccagg ctgtctatat attacacatc tacattacag 240
caggcatcc catcaagggtt cagtggaaat gggctcggga gagattatct cctcagcatc 300
agaaacctgg agcctgaaga tattgcaact tattattgtc aacagtatga taattctcca 360
ttgacgtttc gctcggggac aaagttggaa ataaaaacgg gtggcggtgg ctcgggcggt 420
gggtgggtcg gtggcgggcg atctgatgta cagcttcagg agtcaggacc tggcctcgtg 480
aaactgttct agtcttctgc tctcacctgc tctgtcactg gctactccat caccagtggt 540
ttctacttga actggtatcg acagtttccg ggaacacaaa tggaaatggat gggtccacata 600
agccacgacg gttaggaataa ctacaacca tctctcataa atcgaatctc catcactcgt 660
gacacattta agaaccagtt ttctctgaag ttgagttctg tgactactga ggacacagct 720
acatatttct gtgcaagaca ctacggtagt acgggaagcta tggactactg gggtcaacgga 780
acctcagcta ccgtctctct tgatctggag cccaaattct ctgacaaaac tcacacatcc 840
ccacgctccc cagcacctga actctctggg ggatcgctcag tcttctctct cccccaaaa 900
cccaaggaca cctcatgat ctcccggacc cctgaggtca catgcgttgtt ggtggacgtg 960
agccacgaag acctgaggt caagttcac tggtagctgg acggcgtgga ggtgataat 1020
gccaaacaaa agccgcggga ggagcagtat aacagcacgt accgtgttgt cagctctc 1080
acctctctgc accagagctg gctgaatggc aaggagtaaca agtccaaggt ctccaacaaa 1140
gccctcccaag ccccatcaga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 1200
caggtgtata ccttcgtccc atcccgggat gagctgacca agaaccaggt cagcctgacc 1260
tgctcgtgta aaggcttcta tcccagcgac atcgccgtgg agtgggagag caatggcgag 1320
ccgagaacca actacaagac cagcgtctcc gtgtcggact ccgacggctc cttcttctcc 1380
tacagcaagc tcaacgtgga caagagcagg tggcagcagg ggacgctct ctatgctccc 1440
gtgatgcatt aggtcttgca caaccactac acgcagaafa gcctctccct gtctccgggt 1500
aaagcgagat cttcgaaact gctcccatcc tgggccatta ccttaattc gtctaaatgt 1560
atttttggta tatgtgcctt gactcactgc ttgtcccaaa gatgcagaga gagaaggagg 1620
aatgagagat tgagaaggga aagtgtacgc cctgtataaa tcgat 1665

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<210> 270
<211> 550
<212> PRT
<213> Artificial sequence

<220>
<223> fusion polypeptide

<400> 270
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Val Asp Ile Gln Met Thr Gln Ser Pro Ser
20 25 30
Ser Leu Ser Ala Ser Leu Gly Gly Lys Val Thr Ile Thr Cys Lys Ala
35 40 45
Ser Gln Asp Ile Lys Lys Tyr Ile Gly Trp Tyr Gln His Lys Pro Gly
50 55 60
Lys Gly Pro Arg Leu Leu Ile Tyr Tyr Thr Ser Thr Leu Gln Pro Gly
65 70 75 80
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Leu
85 90 95
Ser Ile Arg Asn Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln
100 105 110
Gln Tyr Asp Asn Leu Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu
115 120 125
Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
130 135 140
Gly Ser Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro
145 150 155 160
Ser Gln Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr
165 170 175
Ser Gly Phe Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu
180 185 190
Glu Trp Met Gly His Ile Ser His Asp Gly Arg Asn Asn Tyr Asn Pro
195 200 205
Ser Leu Ile Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln
210 215 220
Phe Phe Leu Lys Leu Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr
225 230 235 240
Phe Cys Ala Arg His Tyr Gly Ser Ser Gly Ala Met Asp Tyr Trp Gly
245 250 255
Gln Gly Thr Ser Val Thr Val Ser Ser Asp Leu Glu Pro Lys Ser Ser
260 265 270
Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly
275 280 285
Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
290 295 300
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
305 310 315 320
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
325 330 335
His Asn Ala Lys Thr Lys Pro Arg Glu Gln Tyr Asn Ser Thr Tyr
340 345 350
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
355 360 365
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
370 375 380
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
385 390 395 400
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
405 410 415
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
420 425 430
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
435 440 445
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
450 455 460
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
465 470 475 480
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
485 490 495
Pro Gly Lys Ala Asp Pro Ser Asn Leu Leu Pro Ser Trp Ala Ile Thr
500 505 510
Leu Ile Ser Val Asn Gly Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys
515 520 525
Phe Ala Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg
530 535 540
Glu Ser Val Arg Pro Val
545 550

<210> 271
<211> 1653
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 271
atgttgatata catctcagct ccttgggctt ttactcttct ggatttcagc ctccagaagt 60
gacatagtgc tgactcagac tccagccact ctgtctctaa ttcttggaga aagagtccaca 120
atgacctgta agaccagtc gaattattggc acaattcttae actggtatca ccaaaaaacca 180
aaggaggctc caaggogctc catcaagatc gcttcgcagt ccattctctgg gatccccctcc 240
agattcagtg ggaattgggtt ggaaacagat ttcaactctca gcatcaataa cctggagactc 300
gattgatactg gaatttattata ctgtcaacaa agtagaagct ggctgtcac gtcgggtctc 360
ggcaccgaag cgagataaaa acggggtggc ggtggctcgg gcggaggtgg gtcgggtggc 420
ggcggatctc aggtcaagct gcagcagctc ggttctggaac tagggaaacc tggggcctca 480
gtgaaactgt cctgcaagac ttacagctac atattcacag atcattatat ttcttgggtg 540
aaacagaagc ctggagaagc cctgcagctg atagaaaatg tttatgtgtg aaatgtgtgt 600
acaagctaca atcaaaaatt ccagggcgaag gccacactga ctgtagataa aatctctagc 660
acagcttaca tgggaactcag cagcctgaca tctgaggatt ctgccatcta ttactgtgca 720
agaaggccgg tagcgacggg ccattgctatg gactactggg gtcaggggat ccaagtacc 780
gtctctctctg atctggagcc caaatcttct gacaaaaact acacatcccc accgtcccca 840
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ctcatgtatc cccggacccc tgaggtcaca tgcgtgtgtg tggagctgag ccacgaagac 960
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ccgoggagg agcagtacaa cagacagtac ggtctgtgtca ggtctctcac cgtcctgcac 1080
caggaactggc tgaattggcaa ggaatcacaag gtgcaaggct ccaacaaagc cctccagctc 1140
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accgttggaca agagcaggtg gcagcagggg aacgttctct catgtctcgt gatgcagtag 1440
gctctgcaca accatctcac gcagaagagc ctctccctgt ctccgggtaa agcgaatctc 1500
tcgaactctg tcccatctct ggccattacc ttaattctcag taaatggaa ttttggata 1560
tgctgcctga cctactgctt tgcccacaaga tgcagagaga gaaggaggaa tgagagattg 1620
agaaggagaa gtgtacgccc tgtataaatc gat
1653

<210> 272
<211> 548
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 272
Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser
1 5 10 15
Ala Ser Arg Ser Asp Ile Val Leu Thr Gln Thr Pro Ala Thr Leu Ser
20 25 30
Leu Ile Pro Gly Glu Arg Val Thr Met Thr Cys Lys Thr Ser Gln Asn
35 40 45
Ile Gly Thr Ile Leu His Thr Tyr His Gln Lys Pro Lys Glu Ala Pro
50 55 60
Arg Ala Leu Ile Lys Tyr Ala Ser Gln Ser Ile Pro Gly Ile Pro Ser

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 65 70 75 80
 Arg Phe Ser Gly Ser Gly Ser Glu Thr Asp Phe Thr Leu Ser Ile Asn
 85 90 95
 Asn Leu Glu Pro Asp Asp Ile Gly Ile Tyr Tyr Cys Gln Gln Ser Arg
 100 105 110
 Ser Trp Pro Val Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys Arg
 115 120 125
 Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln
 130 135 140
 Val Lys Leu Gln Gln Ser Gly Ser Glu Leu Gly Lys Pro Gly Ala Ser
 145 150 155 160
 Val Lys Leu Ser Cys Lys Thr Ser Gly Tyr Ile Phe Thr Asp His Tyr
 165 170 175
 Ile Ser Trp Val Lys Gln Lys Pro Gly Glu Ser Leu Gln Trp Ile Gly
 180 185 190
 Asn Val Tyr Gly Gly Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe Gln
 195 200 205
 Gly Lys Ala Thr Leu Thr Val Asp Lys Ile Ser Ser Thr Ala Tyr Met
 210 215 220
 Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys Ala
 225 230 235 240
 Arg Arg Pro Val Ala Thr Gly His Ala Met Asp Tyr Trp Gly Gln Gly
 245 250 255
 Ile Gln Val Thr Val Ser Ser Asp Leu Glu Pro Lys Ser Ser Asp Lys
 260 265 270
 Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser
 275 280 285
 Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 290 295 300
 Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 305 310 315 320
 Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 325 330 335
 Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 340 345 350
 Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 355 360 365
 Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 370 375 380
 Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 385 390 395 400
 Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
 405 410 415
 Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 420 425 430
 Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Val Leu
 435 440 445
 Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 450 455 460
 Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 465 470 475 480
 Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 485 490 495
 Lys Ala Asp Pro Ser Asn Leu Leu Pro Trp Ala Ile Thr Leu Ile
 500 505 510
 Ser Val Asn Gly Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala
 515 520 525
 Pro Arg Cys Arg Glu Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser
 530 535 540
 Val Arg Pro Val
 545

<210> 273
 <211> 1521
 <212> DNA
 <213> Artificial Sequence
 <220>

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
<223> fusion polynucleotide

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<400> 273
aagcttgccg ccattggatt tcaagtgcag attttcagct tcctgctaatt cagtgcctca 60
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ccaggggaga aggttcaaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg 180
taccagcaga agccaggatc ctgccccaac ccttggaatt atgcccacac caacctggct 240
cttgaggttc aggtctgaag tctgtccagg tattaactgc cctcttactc tctcaaatc 300
agcagagtgg aggtctgaag caagtggagc ctgaaaggag gccagtgtag accagtgtag 360
ccacgttgcg gtgctgggac ctctcaggct tatctaacg cgtctgggct gggcggtgg 420
ggatctggag aggcctgggg cctcagtgaa gatgtcctg aagcctctg gctctggggc ttgactgtg 480
aggtctggag aatattgcact gggtaaaaca gacacctaga cagggcctg aatggattg agctattat 500
ccaggaaatg gtgatactc ctacaatcag aagttcaagg gcaagccac actgactgt 600
gacaaatcct ccagcacagc ctacatgcag ctacagcagg tgacatttga agactctgc 720
gtctatttct gtgcaagagt gggttactat agtaactctt actggtactt cgtgctctgg 780
ggcacaggga ccacggtcac cgtctcttct gatcaggagc ccaaatcttc tgacaaact 840
cgcacattcc caccgtcccc agcacctgaa ctctggggg gaccgtcagt ctctctctc 900
ccccaaaac ccaaggacac cctcatgatc tcctggacc ctgagggtc atgctgtgtg 960
gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga gcgcgtggag 1020
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agctctctca cctctccagg ctgaaatgga aggagtacaa gtgcaaggtc 1140
tccaacaaag aggtgtacac ccccatctag aaaaacatct ccaagaccaa agggcagccc 1200
cgagaaccac agcctgacct gacctgtcaa aggtctctat ccagcgata agctgaccaa gaaccaggtc 1260
aattggggcag cgagagaaca ctacaagacc acgctctcgc tcgctgtgga gtcggagagc 1320
ttcttctctt acagcaagct caccgtggag aagagcaggt ggcacaggg gaacctcttc 1380
tcattgtcgc tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccttc 1440
ctccgggtta aatgatctg a

```

<210> 274

<211> 500

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 274

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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
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Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20      25      30
Leu Ser Ala Ser Pro Gly Glu Lys Val Trp Met Thr Cys Arg Ala Ser
35      40      45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50      55      60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65      70      75      80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85      90      95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100      105      110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115      120      125
Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
130      135      140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145      150      155      160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165      170      175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180      185      190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195      200      205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
210      215      220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225      230      235      240

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<220>
<223> oligo to make IgG hinge CSS mutant using IgG hinge
      SSS as a template
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<400> 277
gtgttgatc aggagcccaa atcttgtagc aaaactcac      39

<210> 278
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligo to amplify constant regions for creating
      IgG hinge mutatnts

<400> 278
gtgtttcta gatcatttac ccggagacag ggagaggctc ttctgcgtgt ag      52

<210> 279
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligo that mutates VH11 L to S

<400> 279
ggaggtggga gctctcaggc ttatctacag cagtctgggg ctgagtcggt gaggcc      56

<210> 280
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligo for amplifying IgG1 constant regions

<400> 280
gtctctagac tatcatttac ccggagacag      30

<210> 281
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' oligo for first PCR to insert IgA hinge into
      IgG1 CH2-CH3

<400> 281
ccatctccct caactccacc taccatctct cctcatgcg cacctgaact cctg      54

<210> 282
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' oligo for second PCR to insert IgA hinge into
      fused to IgG1 CH2

<400> 282
gtgttgatc agccagttcc ctcaactcca cctaccccat ctccccaact      50

<210> 283
<211> 1536
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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cagggggaga aggtgacaat gacttgacag gccagctcaa gtgtaagtta catgcaactgg 180
taccagcaga agccaggatt ctccccaaaa ccctggattt atgccccatc caactctgggt 240
tctggagtcct ctgtctgctt cagtyggcagt gggctctggga cctcttaact tctcacaaatc 300
agcagagtgg aggtcgaaaga tgcctgcaact tattactgcc agcagtggaag tttaacacca 360
cccaagcttcg gtgctgggag caagctggag ctgaagaatg gcgttggttc gggcgtgtgt 420
ggatctggag gaggctggag ctctcaggct tatctacagc agtctggggc tgaactgtgt 480
aggcttgggg cctcagtgaa gatgtctctg aaggtctctg gctacacact tccagttgt 540
aataatgcact gggtaaacga gacacctaga cagggtctgg aatggattgg agctatttat 600
ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660
gacaaatcct ccagcacagc ctacatgcag ctacagcagc tgacatctga agactctgcg 720
tctattttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctcg 780
ggcacaggga ccacgggtcac cgtctctgat cagccagttc cctcaactcc acctaccaca 840
tctccctcaa ctccacctac ccatctccc tcatgcgcac ctgaaactct ggggggacgg 900
tcagtcttcc tcttcccccc aaaaccacaag gacacctca tgatctccg gccctctgag 960
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acgtatccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 1140
tacaagtcca aggtctccaa caaagccctc ccagcccca tcgagaaaac aatcttccaaa 1200
gccaaaggcg agccccgaga accacagggt gactctgctg gtcaaaagct tctatcccg gcagatgct 1260
accaagaacc aggtcagcct gactctgctg gactctgctg aaactccag gcacatgct 1320
gtggagtggg agagcaatgg gcagtcaggag aactccagc agaccacgc tccctgctg 1380
gaactcgaag gctctctctt ctctacagc aagctcacgc tggacaagag caggtggcag 1440
caggggaaag tcttctcatg ctccgtgatg catggagctc tgcacaacca ctacacgag 1500
aagagcctct ccctgtctcc gggtaaatga tctaga 1536
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<210> 284
<211> 505
<212> PRT
<213> Artificial Sequence
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```
<220>
<223> fusion polypeptide
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<400> 284
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 10 15
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125
Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
130 135 140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145 150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165 170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
210 215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225 230 235 240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
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<http://www.uspto.gov/patents>

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245 250 255

Gly Thr Gly Thr Val Thr Val Ser Asp Gln Pro Val Pro Ser Thr
260 265 270 275

Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys
280 285 290 295

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
300 305 310 315 320

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
325 330 335 340 345

Val Asp Gly Val Glu Val His Asn Val Lys Thr Lys Pro Arg Val Leu Glu
350 355 360 365 370 375

Gln Tyr Asn Ser Thr Tyr Arg Val Tyr Lys Cys Lys Val Ser Asn Lys
380 385 390 395 400 405

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
410 415 420 425 430 435

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
440 445 450 455 460 465

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
470 475 480 485 490 495

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
500 505 510 515 520 525

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
530 535 540 545 550 555

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
560 565 570 575 580 585

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
590 595 600 605 610 615

Lys Ser Leu Ser Leu Ser Pro Gly Lys

<210> 285
<211> 1584
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 285
aagcttgccg ccattggatt tcaagtgcag attttcagct tcttgctaatt cagtgcctca 60
gtcataattg ccagaggaca aattgtttct tcccgctctc cagcaatcct gctgcacatc 120
ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagttta catgcactgg 180
taccagcaga agccaggatc ctcccccaaa cctctgattt atgccccatc caactcggtc 240
tctggagctc ctgctgcgtt cagtggcagt gggctgggga cctcttactc tctcacactc 300
agcagagtgg aggctgaaga tgctgccact tattactgcc agcagtggag tttaacca 360
cccacgtctg gtgctgggac caagctggag ctgtacagc tatctacagc gcggtggctc 420
ggattctgag aggtggggag ctctcaggtc gatctctgc aaggctctct gctacacatt taccagttac 480
agccctgggg ctccagtga gacacctaga cagagctcag aagttcaagg acgactgggt 540
aatatgcact gggtaaagca ctacaatcag ctacatgcag ctacagacc agtatactct 600
ccaggaaatg gtgatacttc taccacatct cctctatgct ccaccctccg actgtattat 660
gacaaatctc ccagcacagc ctactcaggt ttcaactgga cgcctcaag tgggaagagc 720
gtctatttct gtcgaagagt ggtgtactat ctacagacc ctgcactgac gacgtctgg 780
ggcacaggga ccacggttac cgtctcttct gatcacagg ttcctcaac tccacttacc 840
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caccgacggg ccctcgaggga cctgtcttta ggttcaagag cgactctcac gtgcacactg 960
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gctgttcaag gaccactgga cgtgacctc tgtggctgct acagcgtgtc cagtgtctct 1080
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tgctgtcccc cgagaaagta cctgactgac catactgcac gggactggaa gaagggggac 1320
gagctgtccc cgtgtgaccag ctagctgcac gctgcactgc gggactggaa gaagggggac 1380
accactctct gcattgtggg ccacgagggc ctgcctgtgg ccttcacaca gaagacatc 1440
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gaccgcttgg cgggtaaac acccatgtgc aatgtgtctg ttgtcatggc ggaggtggac 1560
ggcacttgct actgataatc taga 1584

<210> 286
<211> 520
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 286
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Glu Asp Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125
Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
130 135 140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145 150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165 170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
210 215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225 230 235 240
Ala Arg Val Val Tyr Ser Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245 250 255
Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Pro Val Pro Ser
260 265 270
Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser
275 280 285
Cys Cys His Pro Arg Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu
290 295 300
Leu Leu Gly Ser Glu Ala Ile Leu Thr Cys Thr Leu Thr Gly Leu Arg
305 310 315 320
Asp Ala Ser Gly Val Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys Ser
325 330 335
Ala Val Gln Gly Pro Pro Asp Arg Asp Leu Cys Gly Cys Tyr Ser Val
340 345 350
Ser Ser Val Leu Pro Gly Cys Ala Glu Pro Trp Asn His Gly Lys Thr
355 360 365
Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser Lys Thr Pro Leu Thr Ala
370 375 380
Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu
385 390 395 400
Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr
405 410 415
Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu
420 425 430
Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser
435 440 445
Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr Phe Ala Val Thr Ser Ile

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 450 455 460
 Leu Arg Val Ala Ala Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys
 465 470 475 480
 Met Val Gly His Glu Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile
 485 490 495
 Asp Arg Leu Ala Gly Lys Pro Thr His Val Asn Val Ser Val Val Met
 500 505 510
 Ala Glu Val Asp Gly Thr Cys Tyr
 515 520

<210> 287
 <211> 775
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion polynucleotide

<400> 287
 tgatcagcca gttccctcaa ctccacctac cccatctccc tcaactccac ctaccccatc 60
 tccctcatgc tgcaccccc gactgtcact gcacgcacgc gccctcgagg acctgtcttt 120
 aggttcagaa gcgattcctca cgtgcacact gaccggcctg agagatgcct caggtgtcac 180
 ctccacctgg acgcctctcaa gtgggaagag ccctgtttcaa ggaccacctt accgtgacct 240
 ctgtgctgtc tacagcgtgt ccagttgtct gccggcgtgt gccgagccat ggaaccatgg 300
 gaagaccttc acctgcactg ctgcctacc cagatccaag acccgcctaa ccgcaccct 360
 ctcaaaatcc ggaacacat tccggcccga ggtccacctg ctgccgcgc cgtcgaggga 420
 ctggtgcctg aacgagctgg tgacgtgtgac gtgcctggca cgtgcttca gccccaagga 480
 tgtgtcgtgt cgctggctgc aggggtcaca ggagctgccc ccgagagaat acctgacttg 540
 ggcatccggg caggagccca gccagggcac caccaccttc gctgtgacca gcatactgcg 600
 cgtggcagcc gaggactgga agaaggggga cacttctccc tgcattgttg gccacgagc 660
 cctgcgcgtg gccttcacac agaagaccat cgacgccttg gcgggtaaac ccaccatgt 720
 caatgtgtct gttgtcatgg cggagtgga cggcacctgc tactgataat ctaga 775

<210> 288
 <211> 254
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 288
 Asp Gln Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro
 1 5 10 15
 Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser Leu His Arg
 20 25 30
 Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Ile Leu Thr Cys
 35 40 45
 Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe Thr Trp Thr
 50 55
 Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Asp Arg Asp Leu
 65 70 75 80
 Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys Ala Glu Pro
 85 90 95
 Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser
 100 105 110
 Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg
 115 120 125
 Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn
 130 135 140
 Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp
 145 150 155 160
 Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys
 165 170 175
 Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr
 180 185 190
 Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp Trp Lys Lys
 195 200 205

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu Pro Leu Ala
210 215 220
Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro Thr His Val
225 230 235 240
Asn Val Ser Val Val Met Ala Glu Val Asp Gly Thr Cys Tyr
245 250

<210> 289

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' oligo to PCR IgA hinge-CH2 CH3

<400> 289

gttgtttcta gattatcagt agcagggtgcc gtccacctcc gccatgacaa c

51

<210> 290

<211> 429

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 290

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cgaattattg ttctctgaa caacaggag aatatctctg atcccacctc accattgaga 180
accagatttg tgtaccattt gtctgacctc agctgtaaaa aatgtgatcc tacagaagtg 240
gagctggata atcagatagt tactgctacc cagagcaata tctgtgatga agacagtgct 300
acagagacct gtcactatta tgacagaaac aagtgtcata cagctgtggt cccactcgta 360
tatggtggtg agaccaaata ggtggaaaca gccttaacct cagatgcctg ctatcctgac 420
taatctaga 429

<210> 291

<211> 139

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 291

Arg Ser Gln Glu Asp Glu Arg Ile Val Leu Val Asp Asn Lys Cys Lys
1 5 10 15
Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser Glu Asp Pro Asn
20 25 30
Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val Pro Leu Asn Asn
35 40 45
Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg Thr Arg Phe Val
50 55 60
Tyr His Leu Ser Asp Leu Ser Cys Lys Lys Cys Asp Pro Thr Glu Val
65 70 75 80
Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser Asn Ile Cys Asp
85 90 95
Glu Asp Ser Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg Asn Lys Cys
100 105 110
Tyr Thr Ala Val Val Pro Leu Val Tyr Gly Gly Glu Thr Lys Met Val
115 120 125
Glu Thr Ala Leu Thr Pro Asp Ala Cys Tyr Pro
130 135

<210> 292

<211> 36

<212> DNA

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<213> Artificial Sequence

<220>

<223> 5' oligo to PCR J chain

<400> 292

gtgttagat ctcaagaaga tgaaggatt gttctt 36

<210> 293

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' oligo to PCR J chain

<400> 293

gtgttttcta gattagtcag gatagcaggc atctgg 36

<210> 294

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> 4 carboxy terminal amino acids deleted from IgA
CH3

<400> 294

Gly Thr Cys Tyr
1

<210> 295

<211> 763

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 295

tgatcagcca gtccctctcaa ctccacctac cccatctccc tcaactccac ctaccccatc 60

tcctctcatgc tgcacacccc gactgtcact gcaccgaccg gccctcgagg acctgctctt 120

aggttcagaaa gcgacacctca cgtgcacact gaccggcctg agatagtcct caggtgtcac 180

cttcacctgg acgccctcaa gtgggaagag cgtgtttcaa ggaccacctg acctgacct 240

ctgtggctgc tacagcgtgt ccagtgtcct gccgggctgt gccagacctt ggaaccatgg 300

gaagaccttc acttgcactg ctgcctaccc cgagtccaag acccgctaa ccgccacct 360

ctcaaaatcc ggaacaacat tccggccga ggtccacctg ctgcccgccg cgtcggagga 420

gctggccctg aacgagctgg tgaacgtgac gtgcttgcca cgtggcttca gccccaagga 480

tgtgctgggt cgctggctgc aggggtcaca ggagctgccc cgcgagaagt acctgacttg 540

ggcatcccgg caaggaccca gccagggcac caccactctc gctgtgacca gcatactgcg 600

cgtggcagcg gaagactgga agaaggggga cactctcttc tgcatgggtg gccacgaggc 660

ctgcgcctg gccttcacac agaagacat cgacccttg gcgggtaaac ccacctatgt 720

caatgtgtct gttgtcatgg cggaggtgga ctgataatc aga 763

<210> 296

<211> 250

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 296

Asp Gln Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro

1 5 10 15

Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser Leu His Arg

20 25 30

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50 55 60
Pro Ser Ser Gly Lys Ser Val Gln Gly Pro Pro Asp Arg Asp Leu
65 70 75 80
Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys Ala Glu Pro
85 90 95
Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser
100 105 110
Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg
115 120 125
Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn
130 135 140
Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp
145 150 155 160
Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys
165 170 175
Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr
180 185 190
Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp Trp Lys Lys
195 200 205
Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu Pro Leu Ala
210 215 220
Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro Thr His Val
225 230 235 240
Asn Val Ser Val Val Met Ala Glu Val Asp
245 250

<210> 297

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' oligo for construct with 4 amino acid deletion
in IgA CH3

<400> 297

gtgtgttctca gattatcagt ccacctccgc catgacaaca gacac

45

<210> 298

<211> 1572

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 298

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ccaggggaga aggtcacaat gactgtcagg gccagctcaa ggtgaagtta catgcaactgg 180
taccagcaga agccaggatc ctcccacaaa cctcgattt atgcccacac caacctggct 240
tcttgagctc ctgctcgctt cagtggcagt ggcctgggga cctcttactc tctcaaatc 300
agcagagtgg agcctgaaga tgctgcact tattactgcc agcagtggag tttaacca 360
cccacgtctg gtgctgggac caagctggag ctctacagc agtctggggc ggcggtgggt 420
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggtg 480
agcgtctggg cctcagtgaa gatgtcctgc aaggcttctg gctacacatt tacagttac 540
aatatgcact gggtaagaca gacacctaga cagggcctgg aatggattgg agctatttat 600
ccaggaaatg gtgatacttc ctacaatcag aagttaacgg gcaaggccac actgactgta 660
gacaaatcct ccagcacagc ctacatgcag ctacagcagc tgacatctga agactctgctg 720
gtctatttct ccagcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780
ggcacaggga ccacggtcac cgtctctctt ctacagccag ttcctcctac tcacactacc 840
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caccagccgg cctcaggaga cctgctctta gttcagaag cgatcctcac gtgcacactg 960
accggcctga gagatgcctt aggtgtcacc ttacctgga gcctctcaag tgggaagacg 1020
gctgttcaag gaccactcta cgtgtacctc tgtgtctgct acagcgtgtc cagtgtcctg 1080

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gagtcacaaga	ccccgcctaac	gcgccacccctc	tcaaaatccg	gaaacacatt	ccggcccgag	1200
gtccacctgc	tgccgcgcgc	gtccgcctga	ctggccctga	acgagctggt	gacgctgacg	1260
tgcttgccac	gtggcttcag	cccccaaggat	gtgctggttc	gctggtctga	ggggtcacag	1320
gagctggccc	gcgagaagta	cctgacttgg	gcattccggc	aggagccag	ccagggcacc	1380
accaccttcg	ctgtgaccag	catactgcgc	gtggcagccg	aggactggaa	gaagggggag	1440
accttctcct	gcattggtggg	ccacgagggc	ctggcgtggt	ccttcacaca	gaagaccatc	1500
cgggctgtg	cgggtaaac	caccatgtc	aattgtgtctg	ttgtcatggc	ggaggtggag	1560
tgataactca	ga					1572

<210> 299
 <211> 516
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 299

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser
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Val	Ile	Ile	Ala	Arg	Gly	Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile
			20					25					30		
Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser
			35					40				45			
Ser	Ser	Val	Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser
			50			55					60				
Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Pro	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro
65			70						75					80	
Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile
			85					90					95		
Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp
			100					105					110		
Ser	Phe	Asn	Pro	Pro	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys
		115					120					125			
Asp	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser
		130				135						140			
Gln	Ala	Tyr	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ala
145			150						155					160	
Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Thr	Thr	Phe	Thr	Ser	Tyr
			165					170						175	
Asn	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Arg	Gln	Gly	Leu	Glu	Trp	Ile
			180					185				190			
Gly	Ala	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr	Ser	Tyr	Asn	Gln	Lys	Phe
		195				200					205				
Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr
		210				215					220				
Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys
225					230				235					240	
Ala	Arg	Val	Val	Tyr	Tyr	Ser	Asn	Ser	Tyr	Trp	Tyr	Phe	Asp	Val	Trp
			245					250					255		
Gly	Thr	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Asp	Gln	Pro	Val	Pro	Ser
			260					265					270		
Thr	Pro	Pro	Thr	Pro	Ser	Pro	Ser	Thr	Pro	Pro	Thr	Pro	Ser	Pro	Ser
		275					280					285			
Cys	Cys	His	Pro	Arg	Leu	Ser	Leu	His	Arg	Pro	Ala	Leu	Glu	Asp	Leu
		290				295					300				
Leu	Leu	Gly	Ser	Glu	Ala	Ile	Leu	Thr	Cys	Thr	Leu	Thr	Gly	Leu	Arg
305					310				315					320	
Asp	Ala	Ser	Gly	Val	Thr	Phe	Thr	Trp	Thr	Pro	Ser	Ser	Gly	Lys	Ser
			325						330					335	
Ala	Val	Gln	Gly	Pro	Pro	Asp	Arg	Asp	Leu	Cys	Gly	Cys	Tyr	Ser	Val
			340					345					350		
Ser	Ser	Val	Leu	Pro	Gly	Cys	Ala	Glu	Pro	Trp	Asn	His	Gly	Lys	Thr
		355					360					365			
Phe	Thr	Cys	Thr	Ala	Ala	Tyr	Pro	Glu	Ser	Lys	Thr	Pro	Leu	Thr	Ala
		370				375					380				
Thr	Leu	Ser	Lys	Ser	Gly	Asn	Thr	Phe	Arg	Pro	Glu	Val	His	Leu	Leu
385					390				395					400	

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Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr
405 410 415
Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu
420 425 430
Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser
435 440 445
Arg Gln Glu Pro Ser Gln Gly Thr Thr Phe Ala Val Thr Ser Ile
450 455 460
Leu Arg Val Ala Ala Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys
465 470 475 480
Met Val Gly His Glu Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile
485 490 495
Asp Arg Leu Ala Gly Lys Pro Thr His Val Asn Val Ser Val Val Met
500 505 510
Ala Glu Val Asp
515

<210> 300

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> 14 amino acids deleted from IgAH-T4 (so that total
of 18 amino acids deleted from wild type Iga CH3

<400> 300

Pro Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp
1 5 10

<210> 301

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' oligo for engineering 14 amino acid from IgA-T4

<400> 301

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45

<210> 302

<211> 709

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 302

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agggtcagaa gcgatctcca cgctgcacact gaccggcctg agagatgcct cagggtgtcac 180
cttcacctgg acgcccctcaa gtgggaagag cctgtgtcaa ggaacacctg acctgtacct 240
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gaagaccttc acctgcactg ctgcctaccr cgagtccaag acccgcctaa ctgcacacct 360
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gctggccctg aacgagctgg tgacgtgac gtgcctggca cgtggcttca gccccaagga 480
tgtgtgtgtt cgctggctgc aggggtcaca ggagctgccc cgcgagaagt acctgacctg 540
gcgcatcccg caggagccca gccaggccac caccaccttc gctgtgacca ccatatcgcg 600
cgtggcagcc gaggactgga agaaggggga cactttctcc tgcattgtgg gccacaggac 660
ctcgcgctg gccctcacac agaagaccat cgaccgcttg gcgggtgaaa 709

<210> 303

<211> 236

<212> PRT

<213> Artificial Sequence

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<220>

<223> fusion polypeptide

<400> 303

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35      40      45
Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe Thr Trp Thr
50      55      60
Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Asp Arg Asp Leu
65      70      75      80
Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys Ala Glu Pro
85      90      95
Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser
100      105      110
Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg
115      120      125
Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn
130      135      140
Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp
145      150      155      160
Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys
165      170      175
Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr
180      185      190
Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp Trp Lys Lys
195      200      205
Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu Pro Leu Ala
210      215      220
Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys
225      230      235

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<210> 304

<211> 1518

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 304

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gacaaattct ccagcacagc ctacatgcag ctacagcagc tgacatctga agactctgct 720
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gaccgcttgg cgggtaaa 1518

<210> 305

<211> 502

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 305

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
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Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Gln Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125
Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
130 135 140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145 150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165 170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
210 215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225 230 235 240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245 250 255
Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Pro Val Pro Ser
260 265 270
Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser
275 280 285
Cys Cys His Pro Arg Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu
290 295 300
Leu Leu Gly Ser Glu Ala Ile Leu Thr Cys Thr Leu Thr Gly Leu Arg
305 310 315 320
Asp Ala Ser Gly Val Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys Ser
325 330 335
Ala Val Gln Gly Pro Pro Asp Arg Asp Leu Cys Gly Cys Tyr Ser Val
340 345 350
Ser Ser Val Leu Pro Gly Cys Ala Glu Pro Trp Asn His Gly Lys Thr
355 360 365
Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser Lys Thr Pro Leu Thr Ala
370 375 380
Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu
385 390 395 400
Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr
405 410 415
Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu
420 425 430
Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser
435 440 445

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
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 Leu Arg Val Ala Ala Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys
 465 470 475 480
 Met Val Gly His Glu Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile
 485 490 495
 Asp Arg Leu Ala Gly Lys
 500

<210> 306
 <211> 924
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion polynucleotide

<400> 306
 gcaacctaca tgatggggaa tgagttgacc ttctatagat attccatctg cacgggcacc 60
 tccagtggaa atcaagtga cctcactatc caaggactga gggccatgga cacgggactc 120
 tacatctgca aggtggagct catgtaccac ccgccatact acctgggcat aggcacacga 180
 acccagattt atgtaattga tccagaaccg tgcccagatt ctgatcaacc caaatcttgt 240
 gacaaaactc acacattgcc accgtgccca gcaactgaac tcctgggggg accgtcagtc 300
 ttctctcttc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 360
 tgcgtgggtg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 420
 ggctgtgagg tgcataatgc caagacaag ccgctggagg agcagtaaca cagcacgtac 480
 cgtgtgttca cgtctctcac cgtctctgac caggactggc tgaatggcaa ggagtacaag 540
 tccaaggtct ccaacaagac ctctccagcc cccatcgaga aaacaatctc caaagccaaa 600
 gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag 660
 aaccaggtca gcctgacctg cctggtcaaa ggcttctat ccagcgacat cgccgtggag 720
 tggggagagca atggggacgc ggagaaacac tacaagacca cgctctccgt ctggactctc 780
 gacggctctc ttctctctta cagcaagctc accgtggaca agagcaggtg gcacgagggg 840
 aacgtctctc catgctccgt gatcgatgag gctctgcaca accactacac gcagaagagc 900
 ctctccctgt ctccgggtaa atga 924

<210> 307
 <211> 382
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 307
 Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
 1 5 10 15
 Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
 20 25 30
 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
 35 40 45
 Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
 50 55 60
 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
 65 70 75
 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
 80 85 90
 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
 100 105 110
 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
 115 120 125
 Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
 130 135 140
 Pro Cys Pro Asp Ser Asp Gln Pro Lys Ser Cys Asp Lys Thr His Thr
 145 150 155 160
 Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
 165 170 175
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 180 185 190

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 195 200 205
 Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 210 215 220
 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 225 230 235
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 245 250 255
 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 260 265 270
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 275 280 285
 Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 290 295 300
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 305 310 315
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Val Leu Asp Ser Asp
 320 325 330
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 335 340 345
 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 350 355 360
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 370 375 380

<210> 308
 <211> 453
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion polynucleotide

<400> 308
 atgggggtac tgctcacaca gaggacgctg ctccagtctgg tccttgacct cctgtttcca 60
 agcatggcga gcatggcaat gcacgtggcc cagcctgctg tggactggcc cagcagccga 120
 ggcacgcga gctttgtgtg tgagtgatga ttcaccaggca aagccactga ggtccgggtg 180
 acagctgcttc ggcaggctga cagccagggtg actgaagctc gtgcggcaac ctacatgatg 240
 gggaatgagt tgaccttctt agatgattcc atctgcacgg gacatccag tgggaatcaa 300
 ttgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcagggtg 360
 gagctcatgt acccaccgcc atactacctg ggcataggca acggaacca gatttatgta 420
 attgatccag aaccgtgccc agattctgat caa 453

<210> 309
 <211> 151
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 309
 Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
 1 5 10 15
 Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
 20 25 30
 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
 35 40 45
 Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
 50 55 60
 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
 65 70 75 80
 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
 85 90 95
 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
 100 105 110
 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Tyr
 115 120 125

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
130 135 140
Pro Cys Pro Asp Ser Asp Gln
145 150

<210> 310
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' oligo for engineering 14 amino acids from
Iga-T4

<400> 310
gttgttgatc agccaggttcc ctcaactcca cctaccccat ctccctcaac t 51

<210> 311
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 311
atgggggtac tgctcacaca gaggacgtg ctcagttcg tccttgact cctgtttcca 60
agcatggcga gcatg 75

<210> 312
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 312
Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
1 5 10 15
Leu Leu Phe Pro Ser Met
20

<210> 313
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 313
gcaatgcacg tggccagcc tgctgtggtta ctggccagca gccgagggat cgccagcttt 60
gttgttgagt atgcattctc aggcacagcc actgaggtcc ggggacagt gcttcggcag 120
gttgacagcc aggtgactga agtctgtgctg gcaacctaca tgacggggaa tgagttgacc 180
ttcttagatg attccattctg caggggcacc tccagtgga atcaagtgaa cttcattac 240
caaggactga cagggcatgga caggggactc tacattctga aggtggagct catgtacca 300
cgccatact acctgggcat aggcacgga acccagattt atgtaatga tccagaaccg 360
tgccagatt ct 372

<210> 314
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<400> 314

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Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly
1      5      10      15
Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu
20      25      30
Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val
35      40      45
Cys Ala Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp Asp
50      55      60
Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile
65      70      75      80
Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu
85      90      95
Leu Met Tyr Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln
100      105      110
Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
115      120

```

<210> 315

<211> 1149

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 315

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atgggggtac tgctcacaca gaggacgctg ctcagctctgg tccttgcaact cctgtttcca 60
agcatgggca gcatggcaat gcacgtggcc cagcctgctg tggactgggc cagcagccga 120
ggcatggcca gctttgtgtg tgagtatgca tctcaggcca aagcactatga ggtccgggtg 180
cagatgcttc ggcaggctga cagccaggctg actgaagtct gtgcggcaac ctacatgatg 240
gggaatgagt tgaccttctc agatgattcc atttgacagg gcacctccag tggaaatcaa 300
gtgaacctca ctgaacctca actgaggagg atggacacgg gactctacat ctgcaaggty 360
gagctcatgt acccaccgcc atactacctg ggcataggca acggaaccca gatttatgta 420
attgatccag aaccgtgcc agattctgat caacccaaat ctctgacaa aactcacaca 480
tccccaccgt cccagaccc tgacctctg gggggatcgt cagtcttctc ctcccccca 540
aaaaccaagg acacctctat gatctcccg gacctctgagg tccatagcgt ggtggtggac 600
gtagccacag aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 660
aatgccaaag caaagcccg gaggagcag tacaacagca cgtaccgtgt ggtcagctc 720
ctcacccgtc tgaccacaga ctggctgaat ggcaaggagt acaagtgcga ggtctccaac 780
aaagccctcc cagcccccac cgagaaaaca atctccaag ccaagggcca gccccgaga 840
ccacaggtgt acacctctgc ccatcccg gtagagctga ccaagaacca ggtcagcctg 900
acctgctctg tcaaaaggctt ctatccacgc gacatcgctg tggagtggga gagcaatggg 960
cagccggaga acaactacaa gaccacgctt cccgtgctgg actccgacgg ctctctcttc 1020
ctctacagca agctcacctt ggacaagagc aggtggcagc aggggaacgt ctctcctc 1080
tcggtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctcgc 1140
ggtaaatga

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<210> 316

<211> 382

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 316

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Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
1      5      10      15
Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
20      25      30
Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
35      40      45
Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
50      55      60
Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
65      70      75      80

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<210> 317
<211> 1221
<212> DNA
<213> Artificial sequence

<220>
<223> fusion polynucleotide

400> 317						
atgggggtagt	tgctcacaca	gaggacgctg	ctcagtcctgg	tccctgcact	ccgtgttcca	60
agcatctggca	gcatgpycaat	gcacgtggcc	cagcctctgtg	tggtactcgc	cagacagccga	120
ggcattcgaca	gctttgttgg	tgagatagta	ttctccagaca	aagcactcata	ggttcggggt	180
acagctctgtc	ggcaggctgca	cagcagctgtg	actgaagtcct	gtgcgcccaac	ctcatgatg	240
gggaattgagt	tgaccttctc	agatgattgt	attctgcagg	cagcctcag	tggaatcac	300
gtgaaactcga	ctatccacgg	actgagggcc	atggacacgg	gactctacat	ctcgaagtg	360
gagctctagt	accaccagag	atactactct	ggcatagaca	acgaaacacca	gatttatgta	420
attgatccag	ctcagctgcc	agattctgtat	cagcaggttc	actcaatcc	acctacccca	480
ttctcccata	ctccactact	cccatctccc	tcattgtgcc	accctcagct	gagctcagc	540
ggcctggcgc	tcgagagctc	gtctctaggt	tcagaagacg	tctccactgt	cacactgac	600
cagctctgag	atggactcag	tgctcactgt	actctggacg	ctcgaagtgt	gaagagcgt	660
gttccacagg	caccttcagg	tgacctctgt	gggtctccgc	gcggtgtcag	tgctctccg	720
gttgctggcg	agcattggaa	ctcagggaag	acctctcact	gcactgtctc	tactcccgcg	780
ctcaagagct	gctctacat	agctccggaa	aacctccgaa	acacattccg	gcccgagctg	840
cactctctgc	cccgccgtc	ggagagagct	acagctgttg	gcagctgttg	gcagagctgc	900
ctctgcctgc	ctctcagcc	caagagagct	ctgtgttcgc	gcagctgttg	gcagctgttg	960
cttcccccgc	agaagtacct	actctgggca	tcccgcctgc	agcccaacga	gggcacatc	1020
acctctctgt	tgaccacgat	gactcgcgtg	gcagcgcagg	actggaagaa	gggggacac	1080
ttctctctga	tggtgtggcca	cagtgctcct	ccgtctggct	tcacaacaa	gaccatcag	1140
cgtctggcgg	gtaaaccac	ccaggtccat	ttgtcttgtt	tcatacggca	gtoaacgcg	1200

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
acctgctact gataatctag a 1221

<210> 318
<211> 403
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 318
Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
1 5 10 15
Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
20 25 30
Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
35 40 45
Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
50 55 60
Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
65 70 75 80
Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
85 90 95
Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
100 105 110
Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
115 120 125
Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
130 135 140
Pro Cys Pro Asp Ser Asp Gln Pro Val Pro Ser Thr Pro Pro Thr Pro
145 150 155 160
Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg
165 170 175
Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu
180 185 190
Ala Ile Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val
195 200 205
Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro
210 215 220
Pro Asp Arg Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro
225 230 235 240
Gly Cys Ala Glu Pro Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala
245 250 255
Ala Tyr Pro Glu Ser Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser
260 265 270
Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Ser Glu
275 280 285
Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly
290 295 300
Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu
305 310 315 320
Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser
325 330 335
Gln Gly Thr Thr Thr Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala
340 345 350
Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu
355 360 365
Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly
370 375 380
Lys Pro Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp Gly
385 390 395 400
Thr Cys Tyr

<210> 319
<211> 1209
<212> DNA
<213> Artificial Sequence

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<220>

<223> fusion polynucleotide

<400> 319

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atgggggttac  tgctcacaca  gaggacgctg  ctccgtctgg  tccttgcact  cctgtttcca  60
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ggcatcgcca  gcttctgtgt  tgagtagtga  ctctccaggca  aagcactaac  ggtccgggtg  180
acagtgcttc  ggcaggctga  cagtcagggt  actgaagctc  gtgcggccaac  ctacatgatg  240
gggaatgagt  tgaccttctc  agatgattcc  actgcacggg  gcacctccag  tggaaatcaa  300
gtgaacctca  ctatccaagg  actgagggcc  atgcacaggc  acggaaccga  gacttatgta  360
gagctcatgt  acccaccgcc  atactacctg  ggcataggca  cctcaactcc  acctaccaca  420
attgatccag  aaccgtgccc  agattctgat  cagccagttc  cctcaactcc  acctaccaca  480
tcttccctcaa  ctccacctac  cccattctcc  tcctgctgcc  accccgact  gtcactgcac  540
cgaccggccc  tcgaggacct  gctcttagtg  tcagaagcga  tcctcacgtg  cacactgacc  600
ggcctgagag  atgcttcagg  tgtcaccttc  acctggagcg  cctcaagtgg  gaagagcgct  660
gttcaaggac  cacctgaccg  tgacctctgt  ggctgctaca  gcgtgtccag  tgtctctgcc  720
ggctgtgccg  agccatggaa  ccatgggaag  accttcactt  gcactgtctg  ctaccaccag  780
tccaagaccc  cgctaaccgc  caccctctca  aaatccggaa  acacttccg  gcccgaggtc  840
caccctgctg  gcgccgcgtc  ggaggagctg  gccctgaacg  agctggtagc  gctgacgtgc  900
ctggcacgtg  gctctcagcc  caaggatgtg  ctggttcgct  ggctgcaggg  gtcacaggag  960
ctgcgccgca  agaagtacct  gacttgggca  tcccgccagg  agcccagcca  gggcaccacc  1020
accttccgtg  tgaccagcat  actgcgcgtg  gcagccgagg  actggaagaa  gggggacacc  1080
ttctcttgca  tgggtggcca  cgaggccctg  ccgctggcct  tcacacagaa  gaccactaac  1140
cgcttggcgg  gtaaacccac  ccatgtcaat  gtgtctgttg  tcattggcga  ggtggactga  1200
taattctaga                                     1209

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<210> 320

<211> 399

<212> PRT

<213> Artificial sequence

<220>

<223> fusion polypeptide

<400> 320

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Met Gly Val  Leu  Leu  Thr  Gln  Arg  Thr  Leu  Leu  Ser  Leu  Val  Leu  Ala
1          5          10          15
Leu  Leu  Phe  Pro  Ser  Met  Ala  Ser  Met  Ala  Met  His  Val  Ala  Gln  Pro
20          25          30          35
Ala  Val  Val  Leu  Ala  Ser  Ser  Arg  Gly  Ile  Ala  Ser  Phe  Val  Cys  Glu
35          40          45          50
Tyr  Ala  Ser  Pro  Gly  Lys  Ala  Thr  Glu  Val  Arg  Val  Thr  Val  Leu  Arg
50          55          60          65
Gln  Ala  Asp  Ser  Gln  Val  Thr  Glu  Val  Cys  Ala  Ala  Thr  Tyr  Met  Met
65          70          75          80
Gly  Asn  Glu  Leu  Thr  Phe  Leu  Asp  Asp  Ser  Ile  Cys  Thr  Gly  Thr  Ser
80          85          90          95
Ser  Gly  Asn  Gln  Val  Asn  Leu  Thr  Ile  Gln  Gly  Leu  Arg  Ala  Met  Asp
100         105         110         115
Thr  Gly  Leu  Tyr  Ile  Cys  Lys  Val  Glu  Leu  Met  Tyr  Pro  Pro  Pro  Tyr
115         120         125         130
Tyr  Leu  Gly  Ile  Gly  Asn  Gly  Thr  Gln  Ile  Tyr  Val  Ile  Asp  Pro  Glu
130         135         140         145
Pro  Cys  Pro  Asp  Ser  Asp  Gln  Pro  Val  Pro  Ser  Thr  Pro  Pro  Thr  Pro
145         150         155         160
Ser  Pro  Ser  Thr  Pro  Pro  Thr  Pro  Ser  Pro  Ser  Cys  Cys  His  Pro  Arg
160         165         170         175
Leu  Ser  Leu  His  Arg  Pro  Ala  Leu  Glu  Asp  Leu  Leu  Leu  Gly  Ser  Glu
175         180         185         190
Ala  Ile  Leu  Thr  Cys  Thr  Leu  Thr  Gly  Leu  Arg  Asp  Ala  Ser  Gly  Val
185         190         195         200
Thr  Phe  Thr  Trp  Thr  Pro  Ser  Ser  Gly  Lys  Ser  Ala  Val  Gln  Gly  Pro
200         205         210         215
Pro  Asp  Arg  Asp  Leu  Cys  Gly  Cys  Tyr  Ser  Val  Ser  Ser  Val  Leu  Pro
215         220         225         230
Gly  Cys  Ala  Glu  Pro  Trp  Asn  His  Gly  Lys  Thr  Phe  Thr  Cys  Thr  Ala
230         235         240         245
Ala  Tyr  Pro  Glu  Ser  Lys  Thr  Pro  Leu  Thr  Ala  Thr  Leu  Ser  Lys  Ser
245         250         255         260

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 260 265 270
 Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu
 275 280 285
 Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Glu
 290 295 300
 Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu
 305 310 315
 Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser
 320 325 330
 Gln Gly Thr Thr Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala
 335 340 345
 Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu
 350 355 360
 Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly
 365 370 375
 Lys Pro Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp
 380 385 390 395

<210> 321
 <211> 328
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion polynucleotide

<400> 321
 cctgaactcc tggggggatc gtcagtcttc ctcttccccc caaaacccaa ggacaccctc 60
 atgatctccc ggaccctga ggtcacatgc gtgggtggg acgtgagcca cgaagacctc 120
 gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataagtcmaa gacaaagccg 180
 cgggaggagc agtacaacag cagctaccgt gtggtcagcg tcctcaccgt cctgcaccag 240
 gactggctga atggcaagga gtacaagtc aaggtctcca acaagaccct ccagccccc 300
 atcgagaaaa ccactcctcaa agccaaag 328

<210> 322
 <211> 109
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 322
 Pro Glu Leu Leu Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro
 1 5 10 15
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 20 25 30
 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 35 40 45
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 50 55 60
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 65 70 75 80
 Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 85 90 95
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 100 105

<210> 323
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acids surrounding the proline at 238

<400> 323

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
1 5 10

<210> 324
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid substitution of Serine for Proline at
238

<400> 324
Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser
1 5 10

<210> 325
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' oligo to PCR IgE Fc

<400> 325
gttgttgatc acgtctgctc cagggaactc acccc 35

<210> 326
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligo to PCR IgE Fc

<400> 326
gttgtttcta gattaacttt taccgggatt tacagacacc gctcgtcg 49

<210> 327
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> oligo to provide open reading frame at carboxy end
of CH4 to read into transmembrane and cytoplasmic
tail of another protein

<400> 327
gttgttttcg aaggatccgc ttaccggga ttacagaca ccgctcgctg g 51

<210> 328
<211> 996
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 328
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cccaggpact atcaacatca cctggctgga ggaacgggcag gtcattggagc tggactttgac 180
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<210> 329
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 329
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 20 25 30
 Leu Cys Leu Val Ser Gly Tyr Thr Pro Gly Thr Ile Ser Thr Trp
 35 40 45
 Leu Glu Asp Gly Gln Val Met Asp Val Asp Leu Ser Thr Ala Ser Thr
 50 55 60
 Thr Gln Glu Gly Glu Leu Ala Ser Thr Gln Ser Glu Leu Thr Leu Ser
 65 70 75 80
 Gln Lys His Trp Leu Ser Asp Arg Thr Tyr Thr Cys Gln Val Thr Tyr
 85 90 95
 Gln Gly His Thr Phe Glu Asp Ser Thr Lys Lys Cys Ala Asp Ser Asn
 100 105 110
 Pro Arg Gly Val Ser Ala Tyr Leu Ser Arg Pro Ser Pro Phe Asp Leu
 115 120 125
 Phe Ile Arg Lys Ser Pro Thr Ile Thr Cys Leu Val Val Asp Leu Ala
 130 135 140
 Pro Ser Lys Gly Thr Val Asn Leu Thr Trp Ser Arg Ala Ser Gly Lys
 145 150 155 160
 Pro Val Asn His Ser Thr Arg Lys Glu Glu Lys Gln Arg Asn Gly Thr
 165 170 175
 Leu Thr Val Thr Ser Thr Leu Pro Val Gly Thr Arg Asp Trp Ile Glu
 180 185 190
 Gly Glu Thr Tyr Gln Cys Arg Val Thr His Pro His Leu Pro Arg Ala
 195 200 205
 Leu Met Arg Ser Thr Thr Lys Thr Ser Gly Pro Arg Ala Ala Pro Glu
 210 215 220
 Val Tyr Ala Phe Ala Thr Pro Glu Trp Pro Gly Ser Arg Asp Lys Arg
 225 230 235 240
 Thr Leu Ala Cys Leu Ile Gln Asn Phe Met Pro Glu Asp Ile Ser Val
 245 250 255
 Gln Trp Leu His Asn Glu Val Gln Leu Pro Asp Ala Arg His Ser Thr
 260 265 270
 Thr Gln Pro Arg Lys Thr Lys Gly Ser Gly Phe Phe Val Phe Ser Arg
 275 280 285
 Leu Glu Val Thr Arg Ala Glu Trp Glu Gln Lys Asp Glu Phe Ile Cys
 290 295 300
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 305 310 315 320
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<210> 330
 <211> 63
 <212> DNA
 <213> Artificial Sequence

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acc 63

<210> 331
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 331
gtgttttcta gatcatttac ccggagacag ggagaggctc ttctgcgtgt ag 52

<210> 332
<211> 91
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 332
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cctgaactcc tgggtggacc gtcagctctc c 91

<210> 333
<211> 1800
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 333
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ccaggggaga aggtcacaat gacttgacag gccagctcaa gtgtaagtta catgcaactgg 180
taccagcaga agccaggatc ctcccccaaa cctctggattt atgccccatc caactcgtgt 240
tctggagctc ctgctcgtct cagtggcagt gggctctggga cctcttactc tctcacaaatc 300
agcagagtgg aggtcgaaga tgctgccact tatctactgcc agcagtgagg ttttaaccca 360
cccacgttcg ggtgtgggac caagctggag ctgaaagggt gcggtggctc gggcggtggt 420
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aatatgcact gggtaaaaga gacacctaga cagggcctgg aatggattgg agctatttat 600
ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660
gacaaatctc ccagcacagc ctacatgcag ctacagaccc tgacatctga agactctgctg 720
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<210> 334
<211> 592
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 334
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Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125
Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
130 135 140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145 150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165 170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
210 215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225 230 235 240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245 250 255
Gly Thr Gly Thr Thr Val Thr Val Ser Asp His Val Cys Ser Arg Asp
260 265 270
Phe Thr Pro Pro Thr Val Lys Ile Leu Gln Ser Ser Cys Asp Gly Gly
275 280 285
Gly His Phe Pro Pro Thr Ile Gln Leu Leu Cys Leu Val Ser Gly Tyr
290 295 300
Thr Pro Gly Thr Ile Asn Ile Thr Trp Leu Glu Asp Gly Gln Val Met
305 310 315 320
Asp Val Asp Leu Ser Thr Ala Ser Thr Gln Glu Gly Glu Leu Ala
325 330 335
Ser Thr Gln Ser Glu Leu Thr Leu Ser Gln Lys His Trp Ser Asp
340 345 350
Arg Thr Tyr Thr Cys Gln Val Thr Tyr Gln Gly His Thr Phe Glu Asp
355 360 365
Ser Thr Lys Lys Cys Ala Asp Ser Asn Pro Arg Gly Val Ser Ala Tyr
370 375 380
Leu Ser Arg Pro Ser Pro Phe Asp Leu Phe Ile Arg Lys Ser Pro Thr
385 390 395 400
Ile Thr Cys Leu Val Val Asp Leu Ala Pro Ser Lys Gly Thr Val Asn
405 410 415
Leu Thr Trp Ser Arg Ala Ser Gly Lys Pro Val Asn His Ser Thr Arg
420 425 430
Lys Glu Glu Lys Gln Arg Asn Gly Thr Leu Thr Val Thr Ser Thr Leu
435 440 445
Pro Val Gly Thr Arg Asp Trp Ile Glu Gly Glu Thr Tyr Gln Cys Arg

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 450 455 460
 Val Thr His Pro His Leu Pro Arg Ala Leu Met Arg Ser Thr Thr Lys
 465 470 475 480
 Thr Ser Gly Pro Arg Ala Ala Pro Glu Val Tyr Ala Phe Ala Thr Pro
 485 490 495
 Glu Trp Pro Gly Ser Arg Asp Lys Arg Thr Leu Ala Cys Leu Ile Gln
 500 505 510
 Asn Phe Met Pro Glu Asp Ile Ser Val Gln Trp Leu His Asn Glu Val
 515 520 525
 Gln Leu Pro Asp Ala Arg His Ser Thr Thr Gln Pro Arg Lys Thr Lys
 530 535 540
 Gly Ser Gly Phe Phe Val Phe Ser Arg Leu Glu Val Thr Arg Ala Glu
 545 550 555 560
 Trp Glu Gln Lys Asp Glu Phe Ile Cys Arg Ala Val His Glu Ala Ala
 565 570 575 580
 Ser Pro Ser Gln Thr Val Gln Arg Ala Val Ser Val Asn Pro Gly Lys
 580 585 590

<210> 335
 <211> 339
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion polynucleotide

<400> 335
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 ccaggaaagg gttctggaatg gatgggaata atatattatg atggaggcac agattataat 180
 tcagcaatta aatccagact gagcatcagc agggacacct ccaagagcca agttttctta 240
 aaaatcaaca gtctgcaaac tgatgcacac gccatgtatt actgtgccag aatccacttt 300
 gattactggg gccaaaggat catggtcaca gtctcctct 339

<210> 336
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion polynucleotide

<400> 336
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 atcacctgcc gtgccagctc cagtgttaagt tacatgtact ggtaccagca gaagtcaggc 120
 gccctccccta aactctggat ttatgcacaca tccaagtctg cttctggagt tccaatcgc 180
 ttcagtggca gtgggtctgg gacctcttat tctctcgcaa tcaacacat ggagactgaa 240
 gatgctgcca ctattactgt tcagcagctg agtagtact cgctcacgtt cgggtctggg 300
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<210> 337
 <211> 785
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion polynucleotide

<400> 337
 aagcttatgg attttcaagt gcagattttc agcttctctc taatcagctc ttcagtcata 60
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 ggggagaagg tcaccatcac ctgccgtggc agctccagtg taagttaact gtactgtgat 180
 cagcagaagt caggcgcttc cctaaactc tggatttatg acacatccaa gctggcttct 240
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gatggaggga cagattataa ttacagaatt aaatccagac tgagcatcag caggagacac 660
tccaagagcc aagttttctt aaaaatcaac agtctgcaaa ctgatgcac agccatgtat 720
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gatca 785

<210> 338
<211> 1491
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 338
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<210> 339
<211> 1645
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 339
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ctcccatcct ggccattatc cttaatctca gtaaatggaa tttttgtgat atgctgcctg 1560
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<210> 340
<211> 1645
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 340
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aaccactaca cgcagaagag cctctccctg tctccgggta aagcggatcc ttcgaaacct 1500
ctcccatcct ggccattatc cttaatctca gtaaatggaa tttttgtgat atgctgcctg 1560
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<210> 341
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 341
Gln Val Gln Leu Lys Glu Ala Gly Pro Gly Leu Val Gln Pro Thr Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Asp
20 25 30
Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Gly Ile Ile Tyr Tyr Asp Gly Gly Thr Asp Tyr Asn Ser Ala Ile Lys
50 55 60
Ser Arg Leu Ser Ile Ser Arg Asp Thr Ser Lys Ser Gln Val Phe Leu
65 70 75 80
Lys Ile Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95
Arg Ile His Phe Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val Ser
100 105 110
Ser

<210> 342
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 342
Asp Ile Val Leu Thr Gln Ser Pro Thr Thr Ile Ala Ala Ser Pro Gly
1 5 10 15
Glu Lys Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
20 25 30
Tyr Trp Tyr Gln Gln Lys Ser Gly Ala Ser Pro Lys Leu Trp Ile Tyr
35 40 45
Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Asn Arg Phe Ser Gly Ser
50 55 60
Gly Ser Gly Thr Ser Tyr Ser Leu Ala Ile Asn Thr Met Glu Thr Glu
65 70 75 80
Asp Ala Ala Thr Tyr Cys Gln Gln Trp Ser Ser Thr Pro Leu Thr
85 90 95
Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 343
<211> 258
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 343
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Thr
20 25 30
Thr Ile Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Arg Ala
35 40 45
Ser Ser Ser Val Ser Tyr Met Tyr Trp Tyr Gln Gln Lys Ser Gly Ala
50 55 60
Ser Pro Lys Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val
65 70 75 80
Pro Asn Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Ala
85 90 95
Ile Asn Thr Met Glu Thr Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
100 105 110
Trp Ser Ser Thr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile
115 120 125
Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
130 135 140
Ser Gln Val Gln Leu Lys Glu Ala Gly Pro Gly Leu Val Gln Pro Thr
145 150 155 160
Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser
165 170 175
Asp Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 180 185 190
 Met Gly Ile Tyr Tyr Asp Gly Gly Thr Asp Tyr Asn Ser Ala Ile
 195 200 205
 Lys Ser Arg Leu Ser Ile Ser Arg Asp Thr Ser Lys Ser Gln Val Phe
 210 215 220
 Leu Lys Ile Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys
 225 230 235 240
 Ala Arg Ile His Phe Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val
 245 250 255
 Ser Ser

<210> 344
 <211> 492
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 344
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Thr
 20 25 30
 Thr Ile Ala Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Arg Ala
 35 40 45
 Ser Ser Ser Val Ser Tyr Met Tyr Trp Tyr Gln Lys Ser Gly Ala
 50 55 60
 Ser Pro Lys Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val
 65 70 75 80
 Pro Asn Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Ala
 85 90 95
 Ile Asn Thr Met Glu Thr Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
 100 105 110
 Trp Ser Ser Thr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile
 115 120 125
 Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
 130 135 140
 Ser Gln Val Gln Leu Lys Glu Ala Gly Pro Gly Leu Val Gln Pro Thr
 145 150 155 160
 Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser
 165 170 175
 Asp Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
 180 185 190
 Met Gly Ile Ile Tyr Tyr Asp Gly Gly Thr Asp Tyr Asn Ser Ala Ile
 195 200 205
 Lys Ser Arg Leu Ser Ile Ser Arg Asp Thr Ser Lys Ser Gln Val Phe
 210 215 220
 Leu Lys Ile Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys
 225 230 235 240
 Ala Arg Ile His Phe Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val
 245 250 255
 Ser Ser Asp Gln Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
 260 265 270
 Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 275 280 285
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 290 295 300
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 305 310 315 320
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 325 330 335
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 340 345 350
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 355 360 365
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

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49076.000004pct2 10.207.655 seq List Text 07.24.03.txt
 370 375 380
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 385 390 395 400
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 405 415
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 420 425 430
 Glu Asn Asn Tyr Lys Thr Thr Pro Val Leu Asp Ser Asp Gly Ser
 435 445
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 450 455 460
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 465 470 475 480
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 485 490

<210> 345
 <211> 543
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 345
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
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 20 25 30
 Thr Ile Ala Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Arg Ala
 35 40 45
 Ser Ser Ser Val Ser Tyr Met Tyr Trp Tyr Gln Gln Lys Ser Gly Ala
 50 55 60
 Ser Pro Lys Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val
 65 70 75 80
 Pro Asn Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Ala
 85 90 95
 Ile Asn Thr Met Glu Thr Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
 100 105 110
 Trp Ser Ser Thr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile
 115 120 125
 Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 130 135 140
 Ser Gln Val Gln Leu Lys Glu Ala Gly Pro Gly Leu Val Gln Pro Thr
 145 150 155 160
 Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser
 165 170 175
 Asp Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
 180 185 190
 Met Gly Ile Tyr Tyr Asp Gly Gly Thr Asp Tyr Asn Ser Ala Ile
 195 200 205
 Lys Ser Arg Leu Ser Ile Ser Arg Asp Thr Ser Lys Ser Gln Val Phe
 210 215 220
 Leu Lys Ile Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys
 225 230 235 240
 Ala Arg Ile His Phe Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val
 245 250 255
 Ser Ser Asp Leu Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
 260 265 270
 Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 275 280 285
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 290 295 300
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 305 310 315 320
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 325 330 335
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 Val³⁴⁰ Leu³⁴⁵ His³⁵⁰ Gln³⁵⁵ Asp³⁶⁰ Trp³⁶⁵ Leu³⁷⁰ Asn³⁷⁵ Gly³⁸⁰ Lys³⁸⁵ Glu³⁹⁰ Tyr³⁹⁵ Lys⁴⁰⁰ Cys⁴⁰⁵ Lys⁴¹⁰ Val⁴¹⁵
 Ser³⁴⁰ Asn³⁴⁵ Lys³⁵⁰ Ala³⁵⁵ Leu³⁶⁰ Pro³⁶⁵ Ala³⁷⁰ Pro³⁷⁵ Ile³⁸⁰ Glu³⁸⁵ Lys³⁹⁰ Thr³⁹⁵ Ile⁴⁰⁰ Ser⁴⁰⁵ Lys⁴¹⁰ Ala⁴¹⁵
 Lys³⁴⁰ Gly³⁴⁵ Gln³⁵⁰ Pro³⁵⁵ Arg³⁶⁰ Glu³⁶⁵ Pro³⁷⁰ Gln³⁷⁵ Val³⁸⁰ Tyr³⁸⁵ Thr³⁹⁰ Leu³⁹⁵ Pro⁴⁰⁰ Pro⁴⁰⁵ Ser⁴¹⁰ Arg⁴¹⁵
 Asp³⁴⁰ Glu³⁴⁵ Leu³⁵⁰ Thr³⁵⁵ Lys³⁶⁰ Asn³⁶⁵ Gln³⁷⁰ Val³⁷⁵ Ser³⁸⁰ Leu³⁸⁵ Thr³⁹⁰ Cys³⁹⁵ Leu⁴⁰⁰ Val⁴⁰⁵ Lys⁴¹⁰ Gly⁴¹⁵
 Phe³⁴⁰ Tyr³⁴⁵ Pro³⁵⁰ Ser³⁵⁵ Asp³⁶⁰ Ile³⁶⁵ Ala³⁷⁰ Val³⁷⁵ Glu³⁸⁰ Trp³⁸⁵ Glu³⁹⁰ Ser³⁹⁵ Asn⁴⁰⁰ Gly⁴⁰⁵ Gln⁴¹⁰ Pro⁴¹⁵
 Glu³⁴⁰ Asn³⁴⁵ Tyr³⁵⁰ Lys³⁵⁵ Thr³⁶⁰ Thr³⁶⁵ Pro³⁷⁰ Val³⁷⁵ Leu³⁸⁰ Asp³⁸⁵ Ser³⁹⁰ Arg³⁹⁵ Trp⁴⁰⁰ Gln⁴⁰⁵ Gln⁴¹⁰
 Phe³⁴⁰ Phe³⁴⁵ Leu³⁵⁰ Tyr³⁵⁵ Ser³⁶⁰ Lys³⁶⁵ Leu³⁷⁰ Thr³⁷⁵ Val³⁸⁰ Asp³⁸⁵ Lys³⁹⁰ Ser³⁹⁵ Arg⁴⁰⁰ Trp⁴⁰⁵ Gln⁴¹⁰ Gln⁴¹⁵
 Gly³⁴⁰ Asn³⁴⁵ Val³⁵⁰ Phe³⁵⁵ Ser³⁶⁰ Cys³⁶⁵ Ser³⁷⁰ Val³⁷⁵ Met³⁸⁰ His³⁸⁵ Glu³⁹⁰ Ala³⁹⁵ Leu⁴⁰⁰ His⁴⁰⁵ Asn⁴¹⁰ His⁴¹⁵
 Tyr³⁴⁰ Thr³⁴⁵ Gln³⁵⁰ Lys³⁵⁵ Ser³⁶⁰ Leu³⁶⁵ Ser³⁷⁰ Leu³⁷⁵ Ser³⁸⁰ Pro³⁸⁵ Gly³⁹⁰ Lys³⁹⁵ Ala⁴⁰⁰ Asp⁴⁰⁵ Pro⁴¹⁰ Ser⁴¹⁵
 Asn³⁴⁰ Leu³⁴⁵ Leu³⁵⁰ Pro³⁵⁵ Ser³⁶⁰ Trp³⁶⁵ Ala³⁷⁰ Ile³⁷⁵ Thr³⁸⁰ Leu³⁸⁵ Ile³⁹⁰ Ser³⁹⁵ Val⁴⁰⁰ Asn⁴⁰⁵ Gly⁴¹⁰ Ile⁴¹⁵
 Phe³⁴⁰ Val³⁴⁵ Ile³⁵⁰ Cys³⁵⁵ Cys³⁶⁰ Leu³⁶⁵ Thr³⁷⁰ Tyr³⁷⁵ Cys³⁸⁰ Phe³⁸⁵ Ala³⁹⁰ Pro³⁹⁵ Arg⁴⁰⁰ Cys⁴⁰⁵ Arg⁴¹⁰ Glu⁴¹⁵
 Arg³⁴⁰ Arg³⁴⁵ Asn³⁵⁰ Glu³⁵⁵ Arg³⁶⁰ Leu³⁶⁵ Arg³⁷⁰ Arg³⁷⁵ Glu³⁸⁰ Ser³⁸⁵ Val³⁹⁰ Arg³⁹⁵ Pro⁴⁰⁰ Val⁴⁰⁵
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<210> 346

<211> 543

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 346

Met¹ Asp⁵ Phe¹⁰ Gln¹⁵ Val²⁰ Gln²⁵ Ile³⁰ Phe³⁵ Ser⁴⁰ Phe⁴⁵ Leu⁵⁰ Leu⁵⁵ Ile⁶⁰ Ser⁶⁵ Ala⁷⁰ Ser⁷⁵
 Val¹ Ile⁵ Met¹⁰ Ser¹⁵ Arg²⁰ Gly²⁵ Val³⁰ Asp³⁵ Ile⁴⁰ Val⁴⁵ Leu⁵⁰ Thr⁵⁵ Gln⁶⁰ Ser⁶⁵ Pro⁷⁰ Thr⁷⁵
 Thr¹ Ile⁵ Ala¹⁰ Ala¹⁵ Ser²⁰ Pro²⁵ Gly³⁰ Glu³⁵ Lys⁴⁰ Val⁴⁵ Thr⁵⁰ Ile⁵⁵ Thr⁶⁰ Cys⁶⁵ Arg⁷⁰ Ala⁷⁵
 Ser¹ Ser⁵ Ser¹⁰ Val¹⁵ Ser²⁰ Tyr²⁵ Met³⁰ Tyr³⁵ Trp⁴⁰ Tyr⁴⁵ Gln⁵⁰ Gln⁵⁵ Lys⁶⁰ Ser⁶⁵ Gly⁷⁰ Ala⁷⁵
 Ser¹ Pro⁵ Lys¹⁰ Leu¹⁵ Trp²⁰ Ile²⁵ Tyr³⁰ Asp³⁵ Thr⁴⁰ Ser⁴⁵ Lys⁵⁰ Leu⁵⁵ Ala⁶⁰ Ser⁶⁵ Gly⁷⁰ Val⁷⁵
 Pro¹ Asn⁵ Arg¹⁰ Phe¹⁵ Ser²⁰ Gly²⁵ Ser³⁰ Gly³⁵ Ser⁴⁰ Gly⁴⁵ Thr⁵⁰ Ser⁵⁵ Tyr⁶⁰ Ser⁶⁵ Leu⁷⁰ Ala⁷⁵
 Ile¹ Asn⁵ Thr¹⁰ Met¹⁵ Glu²⁰ Thr²⁵ Glu³⁰ Asp³⁵ Ala⁴⁰ Ala⁴⁵ Thr⁵⁰ Tyr⁵⁵ Tyr⁶⁰ Cys⁶⁵ Gln⁷⁰ Gln⁷⁵
 Trp¹ Ser⁵ Ser¹⁰ Thr¹⁵ Pro²⁰ Leu²⁵ Thr³⁰ Phe³⁵ Gly⁴⁰ Ser⁴⁵ Gly⁵⁰ Thr⁵⁵ Lys⁶⁰ Leu⁶⁵ Glu⁷⁰ Ile⁷⁵
 Lys¹ Arg⁵ Gly¹⁰ Gly¹⁵ Gly²⁰ Ser²⁵ Gly³⁰ Gly³⁵ Gly⁴⁰ Gly⁴⁵ Ser⁵⁰ Gly⁵⁵ Gly⁶⁰ Gly⁶⁵ Gly⁷⁰ Gly⁷⁵
 Ser¹ Gln⁵ Val¹⁰ Gln¹⁵ Leu²⁰ Lys²⁵ Glu³⁰ Ala³⁵ Gly⁴⁰ Pro⁴⁵ Gly⁵⁰ Leu⁵⁵ Val⁶⁰ Gln⁶⁵ Pro⁷⁰ Thr⁷⁵
 Gln¹ Thr⁵ Leu¹⁰ Ser¹⁵ Leu²⁰ Thr²⁵ Cys³⁰ Thr³⁵ Val⁴⁰ Ser⁴⁵ Gly⁵⁰ Phe⁵⁵ Ser⁶⁰ Leu⁶⁵ Thr⁷⁰ Ser⁷⁵
 Asp¹ Gly⁵ Val¹⁰ His¹⁵ Trp²⁰ Ile²⁵ Arg³⁰ Gln³⁵ Pro⁴⁰ Pro⁴⁵ Gly⁵⁰ Lys⁵⁵ Gly⁶⁰ Leu⁶⁵ Glu⁷⁰ Trp⁷⁵
 Met¹ Gly⁵ Ile¹⁰ Ile¹⁵ Tyr²⁰ Tyr²⁵ Asp³⁰ Gly³⁵ Gly⁴⁰ Thr⁴⁵ Asp⁵⁰ Tyr⁵⁵ Asn⁶⁰ Ser⁶⁵ Ala⁷⁰ Ile⁷⁵
 Lys¹ Ser⁵ Arg¹⁰ Leu¹⁵ Ser²⁰ Ile²⁵ Ser³⁰ Arg³⁵ Asp⁴⁰ Thr⁴⁵ Ser⁵⁰ Lys⁵⁵ Ser⁶⁰ Gln⁶⁵ Val⁷⁰ Phe⁷⁵
 Leu¹ Lys⁵ Ile¹⁰ Asn¹⁵ Ser²⁰ Leu²⁵ Gln³⁰ Thr³⁵ Asp⁴⁰ Asp⁴⁵ Thr⁵⁰ Ala⁵⁵ Met⁶⁰ Tyr⁶⁵ Tyr⁷⁰ Cys⁷⁵
 Ala¹ Arg⁵ Ile¹⁰ His¹⁵ Phe²⁰ Asp²⁵ Tyr³⁰ Trp³⁵ Gly⁴⁰ Gln⁴⁵ Val⁵⁰ Met⁵⁵ Val⁶⁰ Thr⁶⁵ Val⁷⁰
 Ser¹ Ser⁵ Asp¹⁰ Leu¹⁵ Glu²⁰ Pro²⁵ Lys³⁰ Ser³⁵ Asp⁴⁰ Lys⁴⁵ Thr⁵⁰ His⁵⁵ Thr⁶⁰ Ser⁶⁵ Pro⁷⁰
 210 215 220 225 230 235 240 245 250 255

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 260 265 270
 Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val Phe Leu Phe
 275 285
 Pro Pro Lys Pro Lys Asp Thr Thr Met Ile Ser Arg Thr Pro Glu Val
 290 300
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 305 310 315
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 320 335
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 340 345 350
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 355 360 365
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 370 375 380
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 385 390 395 400
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 405 410 415
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 420 425 430
 Glu Asn Asn Tyr Lys Thr Thr Pro Val Leu Asp Ser Asp Gly Ser
 435 440 445
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 450 455 460
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 465 470 475 480
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ala Asp Pro Ser
 485 490 495
 Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly Ile
 500 505 510
 Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg Glu
 515 520 525
 Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
 530 535 540

<210> 347
 <211> 1527
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> fusion polynucleotide

<400> 347
 aagcttatgg attttcaagt cgagattttc agcttctctgc taatcagtcg ttcagtcata 60
 atgtccagag gagtcgacat ccagatgaca cagactacat ctccctctgc tgccttctcg 120
 ggagacagag tcaccatcag ttgcagggca agtcaggagca ttgcgaatta tttaaacctg 180
 tatcagcaga aaccagatgg aactgttaaa ctctcgattct actacacatc aggattacac 240
 tcaggagtc catcaagggt cagtgggcagt gggctctggaa cagattattc tctcaccatt 300
 gccaacctgc tggagcttcg gtggagggca caaactggt tacttttgc aacagggtgaa tacgtcttcg 360
 tggctgtgtg ggtcggatgc cggcggatct accaaacggg agctcggtg cgggtggctg 420
 cctggaactg tgaactctgg agcttcaatg ctccatgagg tccagctgca cagactctga 480
 ggctacatgc tgaactggct gaagcagagc catggaagaa accttgagtg ctcttctact 540
 attaatccat acaaaagtct tactacctac aaccagaaat tcaagggtgaa ggtcgcatta 600
 actgtagaca agtcatccag cacagcctac atggagctcc tcagtctgac atctgaagac 720
 tctgcagctc attactgtgc aagatctggg tactatggtg actcggactg gtactctgat 780
 gtctggggcg caggggaccac ggtcacctgc tctctctgat aggagcccaa atcttctgat 840
 aaaactcaca caaaaccacc gtgccagca cctgaaactc tggggggacc gtcagcttgc 900
 ctcttctccc caaaacccaa ggaacccctc atgatctccc ggacccctga ggtcacatgc 960
 ctggtgtgtg cgttgagcca cgaagacctc gaggtcaagt tcaactggtt cgtggacggc 1020
 gtggagtggt ataatgccaa gacaagaagg cgggaggagc agtacaacag cactgacctg 1080
 gtgtcagcg tctcacgct cctgcaccaa agctggctga atggcaagga gtacaagtgc 1140
 aaggtctcca caagctcca cctgacccct atcgagaaaa caatcttccaa agccaagaagg 1200
 cagccccgag aaccacaggt gtacacctg gggatgagct gaccagaagac 1260
 cgtgcagcgc tgacctgctt ggtcaaaagg ttctatccca gcacatcgc cgtggaggtg 1320
 gagagcaatg ggcagcggga gaacaactac aagaccacgc ctccctgtgc ggtactccag 1380

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaaac 1440
gtcttctcat gtctccgtgat gcatgaggct Ctgacacaacc actacacgca gaagagcctc 1500
tcctctgtctc cgggtaaatg atctaga 1527

<210> 348
<211> 504
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 348
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
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Val Ile Met Ser Arg Gly Val Asp Ile Gln Met Thr Gln Thr Thr Ser
20 25 30
Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala
35 40 45
Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp
50 55 60
Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly
65 70 75 80
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu
85 90 95
Thr Ile Ala Asn Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln
100 105 110
Gln Gly Asn Thr Leu Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Val
115 120 125
Thr Lys Arg Glu Leu Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140
Gly Gly Gly Ser Ile Asp Glu Val Gln Leu Gln Gln Ser Gly Pro Glu
145 150 155 160
Leu Val Lys Pro Gly Ala Ser Met Ser Cys Lys Ala Ser Gly Tyr Ser
165 170 175
Phe Thr Gly Tyr Ile Val Asn Trp Leu Lys Gln Ser His Gly Lys Asn
180 185 190
Leu Glu Trp Ile Gly Leu Ile Asn Pro Tyr Lys Gly Leu Thr Thr Tyr
195 200 205
Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser
210 215 220
Ser Thr Ala Tyr Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala
225 230 235 240
Val Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr
245 250 255
Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Asp Gln
260 265 270
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
275 280 285
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
290 295 300
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
305 310 315 320
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
325 330 335
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Gln
340 345 350
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
355 360 365
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
370 375 380
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
385 390 395 400
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
405 410 415
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
420 425 430
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
435 440 445

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PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr
450 455 460
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
465 470 475
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
485 490 495
Ser Leu Ser Leu Ser Pro Gly Lys
500

<210> 349
<211> 2325
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 349
aagcttgccg ccatggattt tcaagtcgag attttcagct tcctgctaatt cagtgcttca 60
gtcataattg ccagaggaca aattgtctct tcaccagctct cagcaatcct gtctgcatct 120
ccaggaggaa aggtcacaat gactgtcagg gccagctcaa gtgtaaagta catgcaactgg 180
taccagcaga acccaggatt ctcccacaa ccttgattt atgccccatc caactctgctt 240
tctggagtcc ctgctcgctt cagtggtgga gggtctggga cctcttactc tctcacaatc 300
agcagagtgg aggtctgaaga tgctgccact tattactgcc agcagtggag ttttaaccaca 360
cccacgttgc gtgctgggac caagctggag ctgaaaggtg gcggtggctc ggccggtggt 420
ggatctggag gagtggggag ctctcaggct tatctacagc agcttggggc tgaactgtgt 480
agggctgggg cctcagtgaa gatgtcctgc aaggcctctg gctcacattt taccagtgtac 540
aatatgcact gggtaaaaga gacacctaga caggcctctg aatggattgg agctatttat 600
ccaggaaatg gtgatacttc ctacaatcag aagtccaagg gcaaggccac actgactgtta 660
gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgcy 720
gtctattctt gctccaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780
ggcacaggga ccagggctac gctctcttct gatcaatcca actctgaaga agcaaaagaaa 840
gaggaggcca aaaaggaggga agccaagaaa tctaacagcg tcgacattgt tctgactcag 900
tctccaggcca cctctgctgt gactccaggga gataagatct ctcttctcct cagggccagc 960
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<211> 768
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 350
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Leu Ser Ala Ser Pro Gly Glu Lys²⁵ Val Thr Met Thr Cys Arg Ala Ser
35
Ser Ser Val Ser Tyr Met His⁴⁰ Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50
Pro Lys Pro Trp Ile Tyr Ala⁵⁵ Pro Ser Asn Leu Ala Ser Gly Val Pro
65
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr⁷⁰ Ser Tyr Ser Leu Thr Ile
85
Ser Arg Val Glu Ala Glu Asp Ala⁹⁰ Thr Tyr Tyr Cys Gln Gln Trp
100
Ser Phe Asn Pro Pro Thr Phe Gly¹⁰⁵ Ala Gly Thr Lys Leu Glu Leu Lys
115
Gly Gly Gly Gly Ser Gly Gly¹²⁰ Gly Ser Gly Gly Gly Ser Ser
130
Gln Ala Tyr Leu Gln Gln Ser Gly¹³⁵ Ala Glu Leu Val Arg Pro Gly Ala
145
Ser Val Lys Met Ser Cys Lys Ala Ser Gly¹⁵⁰ Tyr Thr Phe Thr Ser Tyr
165
Asn Met His Trp Val Lys Gln Thr¹⁷⁰ Pro Arg Gln Gly Leu Glu Trp Ile
180
Gly Ala Ile Tyr Pro Gly Asn Gly¹⁸⁵ Asp Thr Ser Tyr Asn Gln Lys Phe
195
Lys Gly Lys Ala Thr Leu Thr²⁰⁰ Val Asp Lys Ser Ser Thr Ala Tyr
210
Met Gln Leu Ser Ser Leu Thr Ser²¹⁵ Glu Asp Ser Ala Val Tyr Phe Cys
225
Ala Arg Val Val Tyr²³⁰ Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245
Gly Thr Gly Thr Thr Val Thr Val²⁵⁰ Ser Ser Asp Gln Ser Asn Ser Glu
260
Glu Ala Lys Lys Glu Glu Ala Lys²⁶⁵ Lys Glu Glu Ala Lys Lys Ser Asn
275
Ser Val Asp Ile Val Leu Thr²⁸⁰ Gln Ser Pro Ala Thr Leu Ser Val Thr
290
Pro Gly Asp Arg Val Ser²⁹⁵ Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser
305
Asp Tyr Leu His Trp Tyr Gln Gln³¹⁰ Lys Ser His Glu Ser Pro Arg Leu
325
Leu Ile Lys Tyr Ala Ser His Ser³³⁰ Ile Ser Gly Ile Pro Ser Arg Phe
340
Ser Gly Ser Gly Ser Gly Ser Asp³⁴⁵ Phe Thr Leu Ser Ile Asn Ser Val
355
Glu Pro Glu Asp Val Gly Ile Tyr³⁶⁰ Tyr Cys Gln His His Ser Phe
370
Pro Trp Thr Phe Gly Gly Gly³⁷⁵ Thr Lys Leu Glu Ile Lys Arg Gly Gly
385
Gly Gly Ser Gly Gly Gly Gly³⁹⁰ Ser Gly Gly Gly Ser Gln Ile Gln
405
Leu Val Gln Ser Gly Pro Glu Leu Lys⁴¹⁰ Lys Pro Gly Glu Thr Val Arg
420
Ile Ser Cys Lys Ala Ser Gly Tyr⁴²⁵ Ala Phe Thr Thr Thr Met Gln
435
Trp Val Gln Glu Met Pro Gly⁴⁴⁰ Lys Gly Leu Lys Trp Ile Gly Trp Ile
450
Asn Thr Pro Leu Trp Ser Ala⁴⁵⁵ Lys Ile Cys Arg Arg Leu Gln Gly Arg
465
Phe Ala Phe Ser Leu Glu Thr Ser Ala⁴⁷⁰ Thr Ala Tyr Leu Gln Ile
485
Ser Asn Leu Lys Asp Glu Asp Thr Ala⁴⁹⁰ Thr Tyr Phe Cys Val Arg Ser
500
Gly Asn Gly Asn Tyr Asp Leu Ala⁵⁰⁵ Tyr Phe Ala Tyr Trp Gly Gln Gly
515
Thr Leu Val Thr Val Ser Asp⁵²⁰ Gln Glu Pro Lys Ser Ser Asp Lys Thr
530
His Thr Ser Pro Pro Ser⁵³⁵ Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser
545
550
560

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565 570 575
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
580 585 590
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
595 600 605
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
610 615
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
625 630 635
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
645 650 655
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
660 665 670
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
675 680 685
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
690 695 700
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
705 710 715 720
Ser Asp Gly Ser Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
725 730 735
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
740 745 750 755
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
755 760 765

<210> 351
<211> 1521
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

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ccaggggaga aggtacaat gacttgcagg gccagctcaa gtgtaatga catgcactgg 180
taccagcaga agccaggatc ctccccaaa ccctggattt atgcccact caactggctc 240
tctggagtcc ctgctcgctt cagtggcagg gggctgggga cctcttact tccacaatc 300
agcagagtgg aggtcgaaga tgcctccact tattactgcc agcagtgga ttttaacca 360
ccccagtctg gtctggggac caagctggag ctgaaagatg gcggtggctc gggcggtggt 420
ggatctggag gaagtgggag ctctcaggct tatctacagc agtctggggc tgagctgggt 480
aggctggggg cctcagtgaa gatgtcctgc aaggctctcg gctacacatt taccagttac 540
aatatgcact gggtaaaaga gacacataga caggggctgg aatgattgag agctatttat 600
ccaggaaatg gtgatacttc ctacatcgag ctacatcgag ctacagagcc tgacatctga agactctgcy 720
gacaaaatct ctgcaagagt gtgcagtgac agcacctgaa agtcaactctt agtactctt 780
gtctattctt ctcaggtcac caggtcttct gatcaggagc ccaaatcttc tgacaaaact 840
cacacatccc caccgtccc ccagagcac ctcatgata tccctggggg gatcgctcgt tctctcttc 900
ccccaaaac ccagagcac cctcaggtc aagttcaagg gcaagggcac actgactgta 960
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cgagaaccac aggtgtacac cctgccccca tcccggtgat agctgaccaa gaacaggtc 1260
agcctgacct cctgggtcaa aggtctctat cccagcgaga tcgctgagat gtggagagac 1320
aatgggacag cggagaacaa ctacaagacc acgctctccg tgctggatct cgacggcttc 1380
ttcttctctt acagacaagt caccgtggac aagagcaggt ggacagcagg gaactgtctc 1440
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<210> 352
<211> 500
<212> PRT
<213> Artificial Sequence

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
<220>
<223> fusion polypeptide

<400> 352
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Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125
Asp Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
130 135 140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145 150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165 170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
210 215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225 230 235 240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245 250 255
Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser
260 265 270
Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu
275 280 285
Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
290 295 300
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser
305 310 315 320
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
325 330 335
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
340 345 350
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
355 360 365
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
370 375 380
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
385 390 395 400
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
405 410 415
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
420 425 430
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
435 440 445
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
450 455 460
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
465 470 475 480
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
485 490 495
ser Pro Gly Lys
500

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<210> 353
<211> 423
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<213> Artificial Sequence

<220>
<223> fusion polynucleotide

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tgacacagct ctgtgtttctc attaatcacc tatgctgtac actgggttctg ccagctctcca 180
ggaaagggtc tggagtggct gggagtgata tggagtgggt gaatcacaga ctataatgca 240
ctgtttcatat ccagactgag catcaccaag gacgattcca agagccaagt tttctttaaa 300
atgaacagtc tgcaacctaa tgacacagcc atttattact gtgccagaaa tgggggtgat 360
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tca 423

<210> 354
<211> 366
<212> DNA
<213> qArtificial Sequence

<220>
<223> fusion polynucleotide

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ccaggaagag gctctggagt gctgggagtg atatggagtg gtggaatcac agactataat 180
cgagctttca tatccagact gacatcaccc aaggacgatt ccaagagcca agttttcttt 240
aaaatgaaca gttctgaacc taatgacaca gccatttatt actgtgccag aaatgggggt 300
gataactacc cttattacta tgctatggac tactggggtc aaggaaacct agtcaccgtc 360
tcctca 366

<210> 355
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 355
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gatatttgta tgacgcaggc tgcatctctc aatccagtc cctctggaa ctcagcttcc 120
atctcctcga ggtctagtta gactctccta catagtaatg gcatacctta tttgtattgg 180
tatctgcaga agccaggcca gtctcctcag ctctcgattt atcagatgtc caaccttgcc 240
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<210> 356
<211> 825
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

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tatttgtatt ggtatctgca gaagccaggc cagctctctc agctctcgat tatcagagt 240
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